

GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: October 2, 2006, 16:55:38 ; Search time 17269 Seconds
(without alignments)
11501.574 Million cell updates/sec

Title: US-10-701-263-1

Perfect score: 3106

Sequence: 1 cccgcgagcaagattgtgtg.....ttctcgagcagtgactgc 3106

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : GenBank1*

1: gb_env:*
2: gb_pat:*
3: gb_ph:*
4: gb_pl:*
5: gb_pr:*
6: gb_ro:*
7: gb_sts:*
8: gb_sy:*
9: gb_un:*
10: gb_vl:*
11: gb_ov:*
12: gb_hlg:*
13: gb_in:*
14: gb_cm:*
15: gb_da:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	3106	100.0	3106	5	HUMKGFRA	M80634 Human kerat
2	3013.2	97.0	4574	2	CS115082	CS115082 Sequence
3	3013.2	97.0	4574	2	CS173036	CS173036 Sequence
4	3013.2	97.0	4574	2	DD187137	DD187137 Novel tar
5	2904.2	93.5	4587	2	CS115081	CS115081 Sequence
6	2904.2	93.5	4587	2	CS237527	CS237527 Sequence
7	2904.2	93.5	4587	2	DD187136	DD187136 Novel tar
8	2849.4	91.7	4575	2	CS031438	CS031438 Sequence
9	2849.4	91.7	4575	2	CS040390	CS040390 Sequence
10	2849.4	91.7	4575	2	CS115085	CS115085 Sequence
11	2806.2	90.3	3080	2	DD187140	DD187140 Novel tar
12	2806.2	90.3	3080	5	HUMKGFRA	M80634 Human kerat
13	2806.2	90.3	3080	5	HUMKGFRA	M80634 Human kerat
14	2781.8	89.6	4268	2	AR669919	AR669919 Sequence
15	2781.8	89.6	4268	2	AX334811	AX334811 Sequence
16	2781.8	89.6	4268	2	AX334117	AX334117 Sequence
17	2781.8	89.6	4268	2	AX336422	AX336422 Sequence
18	2781.8	89.6	4268	5	HUMKGFRA	M80634 Human kerat

19	2747.4	88.5	4667	2	CS115090	CS115090 Sequence
20	2747.4	88.5	4667	2	DD187145	DD187145 Novel tar
21	2747.4	88.5	4667	2	AX587545	AX587545 Sequence
22	2728.6	87.8	2923	2	AR669936	AR669936 Sequence
23	2728.6	87.8	2923	2	AB030077	AB030077 Homo sapi
24	2723.4	87.7	2826	2	AR669937	AR669937 Sequence
25	2723.4	87.7	2826	2	AB030078	AB030078 Homo sapi
26	2723.4	87.7	2826	2	AB030075	AB030075 Homo sapi
27	2722	87.6	2868	5	AR669935	AR669935 Sequence
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29	2722	87.6	2868	5	AB030074	AB030074 Homo sapi
30	2722	87.6	2941	2	AR669934	AR669934 Sequence
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33	2714.2	87.4	3415	2	CQ793704	CQ793704 Sequence
34	2674.4	86.1	4142	2	CQ728285	CQ728285 Sequence
35	2639.6	85.0	3219	2	CS115087	CS115087 Sequence
36	2639.6	85.0	3219	2	DD187142	DD187142 Novel tar
37	2556.8	82.3	3248	5	HSRGPFR2MR	Z71829 H.sapiens P
38	2556.8	82.3	3248	5	HSRGPFR2UA	Z69641 H.sapiens f
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40	2506	80.7	3216	2	CS115086	CS115086 Sequence
41	2506	80.7	3216	2	DD187141	DD187141 Novel tar
42	2475	79.7	4310	2	CS115088	CS115088 Sequence
43	2475	79.7	4310	2	DD187143	DD187143 Novel tar
44	2404.4	77.4	4222	2	CS115092	CS115092 Sequence
45	2404.4	77.4	4222	2	DD187147	DD187147 Novel tar

ALIGNMENTS

RESULT 1	HUMKGFRA	3106 bp	mRNA	linear	PRI 27-APR-1993
LOCUS	HUMKGFRA				
DEFINITION	Human keratinocyte growth factor receptor mRNA, complete cds.				
ACCESSION	M80634				
VERSION	M80634.1 GI:186740				
KEYWORDS	keratinocyte growth factor receptor.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	1 (bases 1 to 3106)				
AUTHORS	Waki,T., Bottaro,D.P., Fleming,T.P., Smith,C.L., Burgess,W.H., Chan,A.M. and Aaronson,S.A.				
TITLE	Determination of ligand-binding specificity by alternative splicing: two distinct growth factor receptors encoded by a single gene				
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 89 (1), 246-250 (1992)				
COMMENT	Gene				
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QY 593 GAGTGCCTGCTCTGTTGAAGAATGCGCGTGATCATTTGAAGTGAAGTGGTGAC 652
DB 767 GAGGTGCGTGCCTGTTGAAGAATGCGCGTGATCATTTGAAGTGAAGTGGTGAC 826
QY 653 TTGGGGCCCAACATATGACAGTGTCTTATTTGGGAGTACTTGCAGATTAAGGCGGCA 712
DB 827 TTGGGGCCCAACATATGACAGTGTCTTATTTGGGAGTACTTGCAGATTAAGGCGGCA 886
QY 713 CTTAGAGATCCGGGCTCTATGCTTGAATGAGAGTGTAGACAGTGAACCTTGG 772
DB 887 CTTAGAGATCCGGGCTCTATGCTTGAATGAGAGTGTAGACAGTGAACCTTGG 946
QY 773 TACTTCATGGTGAATGTCACAGATGTCATCTCATCCGAGATGATGACACCGAT 832
DB 947 TACTTCATGGTGAATGTCACAGATGTCATCTCATCCGAGATGATGACACCGAT 1006
QY 833 GGTGCGGAAGATTTTGTCACTGAGAACATGTAACAACAAGAGACATCTTGGACCAAC 892
DB 1007 GGTGCGGAAGATTTTGTCACTGAGAACATGTAACAACAAGAGACATCTGAGCTAAC 1066
QY 893 ACAGAAAAGTGAAGAAAGCGGCTCACTGCTGCTGCGGCAACACTGTCAAGTTTCCG 952
DB 1067 ACAGAAAAGTGAAGAAAGCGGCTCACTGCTGCTGCGGCAACACTGTCAAGTTTCCG 1126
QY 953 TGCCCAAGCGGAGGAGAACCAATGCGAACCATGCGGTGCTGAAAAACGGGAAGATT 1012
DB 1127 TGCCCAAGCGGAGGAGAACCAATGCGAACCATGCGGTGCTGAAAAACGGGAAGATT 1186
QY 1013 AAGCAGAGATGTCATTTGGAAGGCTACAAAGTACGAACCAAGACATGAGGCTCATTTAG 1072
DB 1187 AAGCAGAGATGTCATTTGGAAGGCTACAAAGTACGAACCAAGACATGAGGCTCATTTAG 1246
QY 1073 GAAAGTGTGCTCCCATCTGCAAGGAAATTTATCTGTGATGAGATGATACGAG 1132
DB 1247 GAAAGTGTGCTCCCATCTGCAAGGAAATTTATCTGTGATGAGATGATACGAG 1306
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DB 1307 TCCATCATATCAACGTAACCACTGAGTGTGAGAGGATGCGCTCAACGGCCATCTTC 1366
QY 1193 CAAGCGGACTGCGCGCAATGCTTCAAGTGTGAGAGAGACGTAAGTTTGTCTGC 1252
DB 1367 CAAGCGGACTGCGCGCAATGCTTCAAGTGTGAGAGAGACGTAAGTTTGTCTGC 1426
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DB 1427 AAGGTTTACAGTATGCGGACCAACCATCATCATGATGATCAAGCACTGGAAGAAAGACG 1486
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DB 1487 AGTAATATCGGGCCCGACGGGCTGCGCTACCTCAAGGTTCTCAAGGATCTCGGGATTAAT 1546
QY 1373 AGTTCCATATGCAAGAGTGTGCTGCTTGTCAATGTGACGAGGCGGATGCTGAGGAAATAT 1432
DB 1547 AGTTCCATATGCAAGAGTGTGCTGCTTGTCAATGTGACGAGGCGGATGCTGAGGAAATAT 1606
QY 1433 ATATGTAAGTCTTCAATTTATATAGGAGGAGGCAACCATGTGCTGCTCACTGTCTTG 1492
DB 1607 ATATGTAAGTCTTCAATTTATATAGGAGGAGGCAACCATGTGCTGCTCACTGTCTTG 1666
QY 1493 CCAAAAACAGCAAGCGCTGGAAGAAAGAAAGATTAACAGCTTCCCAAGATCACTGAG 1552
DB 1667 CCAAAAACAGCAAGCGCTGGAAGAAAGAAAGATTAACAGCTTCCCAAGATCACTGAG 1726
QY 1553 ATAGCCATTTATCTGATAGGGGTCTTCTTAATGCGCTGTATGAGTGAATAGCATCTTG 1612
DB 1727 ATAGCCATTTATCTGATAGGGGTCTTCTTAATGCGCTGTATGAGTGAATAGCATCTTG 1786
QY 1613 TGCCGAATGAAGAACAGCAACAGCAAGCAAGCACTTACAGACGCGGCTGTGCAAG 1672
DB 1787 TGCCGAATGAAGAACAGCAACAGCAAGCAAGCACTTACAGACGCGGCTGTGCAAG 1846

QY 1673 CTGACAAAACGTAATGCCCTGCGAGACAGGTAACAGTTTGCGGCTGAGTCCCTCTCC 1732
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QY 1793 CCCATGCTGAGCGGGTCTCCGATATGAACTTCCAGAGAACCCAAATATGGAATTTCCA 1852
DB 1967 CCCATGCTGAGCGGGTCTCCGATATGAACTTCCAGAGAACCCAAATATGGAATTTCCA 2026
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DB 2027 AAGATTAAGCTGACACTGGGCAAGCCCTGGGAGAGGTTGCTTGGGCAATGGTCATG 2086
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QY 2033 ATGAAGATGATGGGAAACAAAGAAATATCATTAATCTTCTGAGACCTGCAACAGAT 2092
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DB 2267 GGGCTCTCTATGTCATATGATGATGATGCTTAAAGGCAACCTCGAATATCTTCGA 2326
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DB 2567 AAAAAACACCAATGGGAGGCTTCCAGTCAAGTGAATGAGTCAAGAACCCCTGTTGAT 2626
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DB 2627 AGAGTATACATCATCATGAGATGATCTGTGCTTTCGGGATGTAATGTGGAGATCTTC 2686
QY 2513 ACTTTAGGGGAGCTGCGCTTACCAAGGATTTCCGTGGAAGAACTTTTAAAGCTGGAAG 2572
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[illegible]

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QY	60	CCAAATCCGAGGCAAGCCCGCGGCGTCAATG - - GCGCTCTTCGCAAGCTTGAGTACGC	116
Db	228	CCAAATCCGA - GCGAGCCCGCGGCGTCAATGCGCGCGCTCTCTCGCAAGCTTGAGTACGC	286
QY	117	G - TGAAGCCGCGGAGGCTTTGGCCCGCGGAAAGACCCAAAGACCACTTTTCTTGCGTTTGA	175
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QY	176	GTTGTCCTCCCGCAACCCCGGGCTGTGCTTTTCTCAATCCGACCCACGCGGAGG - CGGG	234
Db	347	GTTGTCCTCCCAACAACCCCGGGCTGTGCTTTTCTCAATCCGACCCACGCGGAGGCGGG	406
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Db	467	CTCGGTTCTTGAGCCACCGCAGGCTGAAGGCATTGCGCGTATGCTATGCCCTTGAGGA	526
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 2333 AATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2392
 Db 2507 AATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2566
 2393 AAAAGACCAACCAATGAG 2452
 Db 2567 AAAAGACCAACCAATGAG 2626
 2453 AAGATTAACATCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2512
 Db 2627 AAGATTAACATCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2686
 2513 ACTTTAGGAG 2572
 Db 2687 ACTTTAGGAG 2746
 2573 GAAAGACACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2632
 Db 2747 GAAAGACACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2806
 2633 GACTGTGAG 2692
 Db 2807 GACTGTGAG 2866
 2693 GATGCAATTTCTCACTCTCAACCAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2752
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 Db 2927 CAGTATTCACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2986
 2813 TTTTTCGAG 2872
 Db 2987 TTTTTCGAG 3046
 2873 AGTGTAAACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2932
 Db 3047 AGTGTAAACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3106
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 Db 3107 AGTCACTGAG 3166
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 Db 3167 GATCAGAGAGATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3226
 3053 AAAACTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3106
 Db 3227 AAAACTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3280

RESULT 4
 DD187137 4574 bp DNA linear PAT 19-JAN-2006
 LOCUS DD187137
 Novel targets for obesity from subcutaneous fat.
 DEFINITION DD187137.1 GI:85643346
 ACCESSION DD187137.1
 VERSION JP 2005176846-A/27.
 KEYWORDS Homo sapiens (human)
 SOURCE Homo sapiens
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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 1847 CTGACCAACGATATCCCTCGGAGAGACAGTAAAGTTTCGGCTGAGTCCAGCTCTCC 1906
 1733 ATGAATCTCAACACCCCGCTGATGAGATTAACAACCCCTCTCTTCAACCGGACACACC 1792
 1907 ATGAATCTCAACACCCCGCTGATGAGATTAACAACCCCTCTCTTCAACCGGACACACC 1966
 1793 CCCATGCTGAGGAGGATCTCCGAGTATGAATCTTCCAGAGAACCCAAATAGGAGTTTCCA 1852
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 2027 AGAGATTAAGCTGACACTGGGCAAGCCCTGGAGAAAGTTGCTTTGGGCAAGTGTCTATG 2086
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 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homidae; Homo.

REFERENCE
 AUTHORS Clerc, R.G., Duchateau-Nguyen, G., Gardes, C., Mirah, J., and
 Ostenson, C.G.
 TITLE Novel targets for obesity from fat tissue
 JOURNAL Patent: EP 1548445-A 38 29-JUN-2005;
 F. Hoffmann-La Roche AG (CH); Claes-Goran Ostenson (SE)
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ACCESSION CS237527.1 GI:84364558
VERSION CS237527.1 GI:84364558
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SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.

REFERENCE
1. Jin, P.
AUTHORS Patent: WO 2005113596-A 242 01-DEC-2005;
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 REFERENCE 1 (bases 1 to 4587)

AUTHORS Ostenson, C., Clarc, R.G., DuchateauNguyen, G., Gardes, C. and Mizrahi, J.
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 JOURNAL Patent: JP 2005176846-A 26 07-JUL-2005;
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 PD 07-JUL-2005
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 Homidae; Homo.
 REFERENCE
 AUTHORS Abbas, A.; Clark, H.; Ouyang, W.; Williams, M. P.; Wood, W. I. and Wu, T. D.
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REFERENCE
1 Abbas, A., Clark, H., Ouyang, W., Williams, P. M., Wood, W. I. and Wu, T. D.
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Best Local Similarity 96.5%; Pred. No. 0;
Matches 3020; Conservative 0; Mismatches 71; Indels 38; Gaps 9;

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KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.

REFERENCE
1 Clerc, R.G., Duchateau-Nguyen, G., Gardes, C., Mizrahi, J. and Ostenson, C.G.
Novel targets for obesity from fat tissue
Patent: EP 154845-A 42 29-JUN-2005;
F. Hoffmann-La Roche AG (CH); Claes-Goran Ostenson (SE)

TITLE
JOURNAL
F. Hoffmann-La Roche AG (CH); Claes-Goran Ostenson (SE)

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ORIGIN

Query Match 91.7%; Score 2849.4; DB 2; Length 4575;
Best Local Similarity 96.5%; Pred. No. 0;
Matches 3020; Conservative 0; Mismatches 71; Indels 38; Gaps 9;

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VERSION	DD187140.1 GI:85643349			
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SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens			
REFERENCE	Eukaryotic; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
AUTHORS	Mammalia; Euteria; Euarchontoglires; Primates; Catarrhini;			
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JOURNAL	1 (bases 1 to 4575)			
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	Best Local Similarity 96.5%; Pred. No. 0;			
	Matches 3020; Conservative 0; Mismatches 71; Indels 38; Gaps 9;			
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OY		117	G-TGAAGCCCGGAGAGCTTTGGCGCGCGGAGAGACCAGAGCACTCTTCGCGTTTGA	175
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QY	953	TGCCCAAGCCGGGGGGAACCCCAATGCGAACCATGCGGTGGCTGGAAGAAAACGGGAAGAAGTTT	1012
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QY	1013	AAGCAGAGCATGCGATTGGAGGCTACAAAGGTACGAACACAGCACTGAGGCGCTCATTTATG	1072
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O	y	1718	GAGTTCAGCTCTCTCATGAATCTCCAAACCCCGCTGGTAGATTAACAACCGCTCTCT	1777
D	b	1893	GAGTTCAGCTCTCTCATGAATCTCCAAACCCCGCTGGTAGATTAACAACCGCTCTCT	1952
O	y	1778	TCAACGGGACGACCCCCATGCTGGGAGGGGTCTCCAGATATGAATTTCCAGAGAGACCA	1837
D	b	1953	TCAACGGGACGACCCCCATGCTGGGAGGGGTCTCCAGATATGAATTTCCAGAGAGACCA	2012
O	y	1838	AAATGAGAGTTTCCAGAGATTAAGCTGACATGAGGCAAGCCCTGGAGAGAGTTGCTTT	1897
D	b	2013	AAATGAGAGTTTCCAGAGATTAAGCTGACATGAGGCAAGCCCTGGAGAGAGTTGCTTT	2072
O	y	1898	GGGCAAGTGTCTATGCGGGAGAGCACTGGGAATTTACAACAACAGCCCAAGAGGCGGTCT	1957
D	b	2073	GGGCAAGTGTCTATGCGGGAGAGCACTGGGAATTTACAACAACAGCCCAAGAGGCGGTCT	2132
O	y	1958	ACCGTGGCCGTGAAGATGTTGAAGAATGATGACCAAGAGAAAGACTTTGATCTGATG	2017
D	b	2133	ACCGTGGCCGTGAAGATGTTGAAGAATGATGACCAAGAGAAAGACTTTGATCTGATG	2192
O	y	2018	TCAAGATGAGATGATGAAGATGATTTGGGAAACACAAGAAATATCATTAATCTTCTTGA	2077
D	b	2193	TCAAGATGAGATGATGATGAAGATGATTTGGGAAACACAAGAAATATCATTAATCTTCTTGA	2252
O	y	2078	GCTTGCACACAGATGGGCTCTCTATGTCTATAGTTAGATGATGCTCTTAAAGGCAACTCT	2137
D	b	2253	GCTTGCACACAGATGGGCTCTCTATGTCTATAGTTAGATGATGCTCTTAAAGGCAACTCT	2312
O	y	2138	GGAAGATACCTCCGAGCGCCGAGGCGCAACCGGGATGAGATCTCTATGACATTAACCGT	2197
D	b	2313	GGAAGATACCTCCGAGCGCCGAGGCGCAACCGGGATGAGATCTCTATGACATTAACCGT	2372
O	y	2198	GTTCCCTGAGAGAGATGACCTTCAAGGACTTGTGTCTATGACCTTACAGCTGGCAGA	2257
D	b	2373	GTTCCCTGAGAGAGATGACCTTCAAGGACTTGTGTCTATGACCTTACAGCTGGCAGA	2432
O	y	2258	CGAGATGAGATCTTGGCTTCCAAAAATGATTTATGATGAGATTTAGACGCCAAGAAATGT	2317
D	b	2433	CGAGATGAGATCTTGGCTTCCAAAAATGATTTATGATGAGATTTAGACGCCAAGAAATGT	2492
O	y	2318	TTGGTAAACAGAAACAAATGTGATGAAAATAGCAGCTTGGACTCGCAGAGATATCAAC	2377

Db 2493 TTGGTACGAAAAAATGTGATGAAATAGACAGACTTTGGACTGCGCCAGATATCAAC 2552
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2553 AATATAGACTATTACAAAAAGACCAACATGGCGGCTTCAAGTCAATGAGTGTCTCA 2612
2438 GAAGCCCTGTTGATGAGTATACATCTCATCAGAGTATGTCTGCTTCCGGGGTTA 2497
2613 GAAGCCCTGTTGATGAGTATACATCTCATCAGAGTATGTCTGCTTCCGGGGTTA 2672
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QY 3098 GTGAGCTGC 3106
Db 3273 GTGAGCTGC 3281

RESULT 12
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LOCUS AR669941 Sequence 25 from patent US 6900053.
DEFINITION AR669941
ACCESSION AR669941
VERSION AR669941.1 GI:67608232
KEYWORDS
ORGANISM Unknown.
SOURCE Unknown.
UNCLASIFIED.
REFERENCE 1 (bases 1 to 3080)
AUTHORS Freier,S.M.
TITLES Antisense modulation of fibroblast growth factor receptor 2 expression
JOURNAL Patent: US 6900053-A 25 31-MAY-2005;
FEATURES ISIS Pharmaceuticals, Inc.; Carlsbad, CA
Location/Qualifiers
Source 1..3080

ORIGIN
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/mol_type="genomic DNA"

QY 1 CCCGAGACAAAGTTGGTGGAGGCAAG -CAAGCTGAAGTCTTCTCTCTGTTCC 59
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QY 60 CCAATTCGAGGAGCGCCGCGGCGTCATG--GCGCTCTCGCAGCTCGGAGTACG 116
Db CCAATTCGAGGAGCGCCGCGGCGTCATGCGCGCTCTCTCGCAGCTCGGAGTACG 305
QY 117 G-TGAAGCCGAGGAGGCTTGGGCGCGGAGAAACCAAGACCACTCTTCTGCGTTTGA 175
Db GCTGAAGCCGAGGAGGCTTGGGCGCGGAGAAACCAAGACCACTCTTCTGCGTTTGA 365
QY 176 GTTGCTCCCGCAACCCCGGCGTGTGCTTTCTTCATATCCGACCCAGCGGCGGCG -CGGG 234
Db GTTGCTCCCGCAACCCCGGCGTGTGCTTTCTTCATATCCGACCCAGCGGCGGCGG 425
QY 366 GTTGCTCCCGCAACCCCGGCGTGTGCTTTCTTCATATCCGACCCAGCGGCGGCGG 425
Db GACCAACAGAGTGGGAGGAGCGTTGCAATTAAGTACTGACAGCAGCAGC -GAGCGCG 293
QY 426 GACCAACAGAGTGGGAGGAGCGTTGCAATTAAGTACTGACAGCAGCAGCAGCAGCGC 485
Db CTGGGTTCTCGAGCCCAACCGGCGTGTGCTTTCTTCATATCCGACCCAGCGGCGG 545
QY 294 CTGGGTTCTCGAGCCCAACCGGCGTGTGCTTTCTTCATATCCGACCCAGCGGCGG 352
Db CTGGGTTCTCGAGCCCAACCGGCGTGTGCTTTCTTCATATCCGACCCAGCGGCGG 485
QY 486 CTGGGTTCTCGAGCCCAACCGGCGTGTGCTTTCTTCATATCCGACCCAGCGGCGG 545
Db 353 AATGTCAGATGGGATTAACGTCACATGAGATTAAGAGAGACCGGGGATGGTATAC 412
QY 546 AATGTCAGATGGGATTAACGTCACATGAGATTAAGAGAGACCGGGGATGGTATAC 605
Db 413 GTAACATGATGAGTGGGAGTGTTCATCTGCTGTGCTGTGATCAATGAGCACTTGG 472
QY 606 GTAACATGATGAGTGGGAGTGTTCATCTGCTGTGCTGTGATCAATGAGCACTTGG 665
Db 472 TCCCTGGCCGCGCCCTCTCTTCAGTTTAAAGTATCAACATTAAGCCAGAGAGCA 532
QY 666 TCCCTGGCCGCGCCCTCTCTTCAGTTTAAAGTATCAACATTAAGCCAGAGAGCA 725
Db 533 CCAACCAATTAACCAATCTTCAACAGAGATTAAGTGGGCGGCGGAGTGGTAT 592
QY 726 CCAACCAATTAACCAATCTTCAACAGAGATTAAGTGGGCGGCGGAGTGGTAT 785
Db 593 GAGGTGCGGCTGCTGTGAAAGATGCGCGCGATCAGTTGGAATGAAGTGGGTGAC 652
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Db 653 TTGGGCGCCCAACATATAGACAGTGTCTTATTTGGGAGTACTTGCATTAAGGCGCCACG 712
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QY 906 CCAAGAGATCCGCGCTCTATGCTTGTACTGCAATTAAGATCTGTGAGCAAGTAACTGG 965
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Db 833 GGTGCGGAAGATTTGTCAGTAGAACAGTAAACAAAGAGACCAATATCTGACCAAC 892
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QY 1086 ACAGAAAGATGAAAGAGCGGCTCCATGCTGTGCGGCGCAACACTGTCAAGTTTCCG 1145
Db 953 TGCCCAAGCGGCGGAGAACCAATGCAACATGCGGTGGCTGAAAAACGGAGAGGTTT 1012

Db 1146 TGCCACCGGGGGGAAACCAATGCCAATGCGGTGCTGAAAAAGGAGGATTT 1205
 Qy 1013 AAGCAGAGCATGCGATTTGAGGCTACAGGTACGAAACGACATGAGCTCTATTATG 1072
 Db 1206 AAGCAGAGCATGCGATTTGAGGCTACAGGTACGAAACGACATGAGCTCTATTATG 1265
 Qy 1073 GAAAGTGTGCTCCATCTGACAAAGGAAATTAATCTGTGTAGTGAATTAATAGGG 1132
 Db 1266 GAAAGTGTGCTCCATCTGACAAAGGAAATTAATCTGTGTAGTGAATTAATAGGG 1325
 Qy 1133 TCCATCATCAACAGTACCACTGATGTTGTGAGAGGATGCTCAACGCGCCATCTC 1192
 Db 1326 TCCATCATCAACAGTACCACTGATGTTGTGAGAGGATGCTCAACGCGCCATCTC 1385
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 Db 1446 AAGGTTTACAGTATGCTCCAGGCTCCCATCCAGTGTGATCAAGCACTGAGAAAGAGGC 1505
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 Qy 1433 ATATGTAAAGTCTTCAATTTATATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1492
 Db 1626 ATATGTAAAGTCTTCAATTTATATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1685
 Qy 1493 CCAAAACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1552
 Db 1686 CCAAAACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1745
 Qy 1553 ATAGCCATTTACTGATAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1612
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 Qy 1613 TGCCGAATGAAACAGACGACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1672
 Db 1806 TGCCGAATGAAACAGACGACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1865
 Qy 1673 CTGACCAAGGATATCCCTGCGGAGACAGGTACAGTTGAGGAGTCCAGTCTCTCC 1732
 Db 1866 CTGACCAAGGATATCCCTGCGGAGACAGGTACAGTTGAGGAGTCCAGTCTCTCC 1925
 Qy 1733 ATGAATCTCAACACCCGCTGTGTGAGATTAACAACGCTCTCTTCAACGCGACAGACC 1792
 Db 1926 ATGAATCTCAACACCCGCTGTGTGAGATTAACAACGCTCTCTTCAACGCGACAGACC 1985
 Qy 1793 CCAATGCTGCGAGGAGTCTCCGAGTATGAATTTCAAGAGACCCAAATGAGAGTTTCCA 1852
 Db 1986 CCAATGCTGCGAGGAGTCTCCGAGTATGAATTTCAAGAGACCCAAATGAGAGTTTCCA 2045
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Db 2226 ATGAAGATGATGGGAAACAGAGATATCATTAATCTTGGAGGCTGACACAGAT 2285
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 Qy 2153 GCGGAGAGCCACCCGAGATGAGATCTCTTAATGACATTAACGTTCTCGAGAGAGAG 2212
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 Db 2886 GATCGAATTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2945
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RESULT 13
 HUMFGR2A 3080 bp mRNA linear PRI 08-NOV-1994
 LOCUS Homo sapiens fibroblast growth factor receptor 2 IIIB (FGR2) mRNA,
 DEFINITION complete cds.
 ACCESSION M97193
 VERSION M97193.1 GI:182566
 KEYWORDS fibroblast growth factor receptor 2; ligand binding.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homidae; Homo.
 REFERENCE 1 (bases 1 to 3080)

Db 1686 CCAAAACAGACAGCCCTGGAGAGAGAAAAGAGATTACAGCTTCCCAAGATCCTGGAG 1745
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 Qy 1673 CTGACCAAAAGTATCCCTGGCGGAGACAGTAAAGTTGGGTGAGTCACTCTCC 1732
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 Qy 1733 ATGAACTCCAAACACCCCGCTGTGTAGAGTAAACAAGCCTCTCTTCAACGGGACACC 1792
 Db 1926 ATGAACTCCAAACACCCCGCTGTGTAGAGTAAACAAGCCTCTCTTCAACGGGACACC 1985
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 Qy 2153 GCCCGAGGCGCACCCGGGATGAGTACTCTTATGACATTAACGCTGTTCTGAGAGACAG 2212
 Db 2346 GCCCGAGGCGCACCCGGGATGAGTACTCTTATGACATTAACGCTGTTCTGAGAGACAG 2405
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 Db 2406 ATGACCTTCAAGAGCTTGTGTCTATGACCTTACAGCTGGCAGAGGCAATGAGTACTTG 2465
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RESULT 14

AR669919 4268 bp DNA linear PAT 13-JUN-2005
 DEFINITION Sequence 3 from patent US 690053.

AR669919 GI:67608210
 VERSION AR669919.1
 KEYWORDS

SOURCE Unknown.
 ORGANISM Unknown.

REFERENCE Unclassified.
 1 (bases 1 to 4268)

AUTHORS Freiler,S.M.
 TITLE

JOURNAL Antisense modulation of fibroblast growth factor receptor 2
 expression
 Patent: US 690053-A 3 31-MAY-2005;

ISIS Pharmaceuticals, Inc.; Carlsbad, CA
 Location/Qualifiers

FEATURES
 source

1..4268
 /organism="unknown"
 /mol_type="genomic DNA"

ORIGIN

Query Match 89.6%; Score 2781.8; DB 2; Length 4268;

Best Local Similarity 97.3%; Pred. No. 0; Mismatches 62; Indels 18; Gaps 5;

Matches 2887; Conservative 0;

Qy 149 CCCAAGGACCACTCTGCGTTTGAGTGTCTCCCGCAACCCCGGGCTGTCGCTTTC 208
 Db 1 CCCAAGGACCACTCTGCGTTTGAGTGTCTCCCGCAACCCCGGGCTGTCGCTTTC 60
 Qy 209 TCCATCCCGAACCCACGCGGGGCGGCGGAGCAACAAGTGGCGAGAGGCTTGCATTC 267
 Db 61 TCCATCCCGAACCCACGCGGGGCGGCGGAGCAACAAGTGGCGAGAGGCTTGCATTC 120
 Qy 268 AAGTACTGACAGACACG-CGACGCGCTTGGTCTGAGCCCAACGCA-GCTGAAGCA 325
 Db 121 AAGTACTGACAGACACGCGGCGAGCGCTGCTGCTTCCAGACCCACGCGAGCTGAAGCA 180
 Qy 326 TTGCGGTATTCATGCGCGGTAGAGGAAGTGCAGATGAGATTAAGTCAACATGAGAG 385
 Db 181 TTGCGGTATTCATGCGCGGTAGAGGAAGTGCAGATGAGATTAAGTCAACATGAGAG 240
 Qy 386 TATGAAGAGAGACCGGGATTTGTACCGTAAACATGCTGAGTGGGTGCTTTCATCTGC 445
 Db 241 TATGAAGAGAGACCGGGATTTGTACCGTAAACATGCTGAGTGGGTGCTTTCATCTGC 300
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QY	508	GATACCACTTAAAGCCAGAAAGACCCAAACCAAAATCAAAATCTCTCAACCAAGAGT	565
Db	361	GATACCACTTAAAGCCAGAAAGACCCAAACCAAAATCTCTCAACCAAGAGT	420
QY	566	TACGTGGCTGGCCAGGGGAGTCCGTAGAGTGGCTGCTGTGTGAAGAAGATGCCGCGT	625
Db	421	TACGTGGCTGGCCAGGGGAGTCCGTAGAGTGGCTGCTGTGTGAAGAAGATGCCGCGT	480
QY	626	ATCAGTTGCACTAAGATGGGGTSCACTTGGGGCCCAACATAGACAGTCTTATTTGGG	685
Db	481	ATCAGTTGCACTAAGATGGGGTSCACTTGGGGCCCAACATAGACAGTCTTATTTGGG	540
QY	686	GAGTACTTGCAGATTAAGAGGGGCCACACCTTAGAACCTCCGGCCCTATAGCTTGAAC	745
Db	541	GAGTACTTGCAGATTAAGAGGGGCCACACCTTAGAACCTCCGGCCCTATAGCTTGAAC	600
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Db	601	AGTAGGACTGTAGACAGTGAACCTTGGTACTTCATGTGTAATGTCAACAGATGCCATCTCA	660
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Db	901	CGAAACCAAGCACTGGAGGCTCTCATTAATGAAAGTGTGTCCCATCTGCAAGGGGAAATAT	960
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RESULT 15
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 LOCUS Sequence 3320 from Patent WO0194629.

DEFINITION AX332811
 AX332811.1 GI:18123445
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homiidae; Homo.

REFERENCE
 AUTHORS Young, P.E., Augustus, M., Carter, K.C., Ebner, R., Endress, G.,
 Horvath, S., Soppet, D.R. and Weaver, Z.
 TITLE Cancer gene determination and therapeutic screening using signature
 gene sets
 JOURNAL Patent: WO 0194629-A 3320 13-DEC-2001;
 FEATURES Avalon Pharmaceuticals (US)
 source Location/Qualifiers

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 /db_xref="taxon:9606"

ORIGIN

Query Match 89.6%; Score 2781.8; DB 2; Length 4268;
 Best Local Similarity 97.3%; Pred. No. 0;
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 Db 1 CCAGAGACCACTCTTCTGCGTTTGAAGTGTCTCCCGCAACCCCGGCTGTGGCTTTC 60
 Qy 209 TCCATCCCGACCCACGCGGGGCG-CGGGGAACAACAGGTGCGGAGAGCGTTGCAATTC 267
 Db 61 TCCATCCCGACCCACGCGGGGCGCGGGAACAACAGGTGCGGAGAGCGTTGCAATTC 120
 Qy 268 AAGTGAAGTGAAGCAGCAGC-CAAGGCGCTCGTTCTTGAAGCCCAACCGCA-CTGAAGGCA 325
 Db 121 AAGTGAAGTGAAGCAGCAGCAGCGGCGCTCGTTCTTGAAGCCCAACCGGAGGCTGAAGGCA 180

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 Db 181 TTGCGGATGTCATCCCGCTAGAGAGATGTGCAGATGGGATTAAGTCCACATGAGAGA 240
 Qy 386 TATGAAAGAGACCGGGGATTTGGTACCGTAAACATGCTGAGCTGGGGTCTTCAATCTGC 445
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 Db 301 CTGGTGTGTGTCACATGCGAACCTTGTCCCTGGCCCGGCTCTTCAAGTTAGTTAG 360
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Search completed: October 2, 2006, 21:52:09
 Job time : 17277 secs

CC progenitor cells. The method comprises identifying one or more genes that
CC are differentially expressed at least 1.8 fold by one or more metanephric
CC mesenchyme cells at a particular stage of embryonic development compared
CC to one or more intermediate mesoderm cells. The method of the invention
CC is useful for identifying a metanephric mesenchyme cell. These cells are
CC useful for in vitro and in vivo generation of renal tissue, and are
CC useful for treating disease such as acute renal failure, kidney
CC transplant dysfunction and/or chronic renal failure. ABC02045-ABC02126
CC represent human genetic markers of metanephric mesenchyme/renal
CC progenitor cells.

XX Sequence 3106 BP; 825 A; 785 C; 843 G; 653 T; 0 U; 0 Other;

Query Match 100.0%; Score 3106; DB 14; Length 3106;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 3106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1441 GGTCTTCAATTAATAGGCAAGCCCAACCAAGTCTGCTGCTCACTGTCTCCCAAAACA 1500
DB 1441 GGTCTTCAATTAATAGGCAAGCCCAACCAAGTCTGCTGCTCACTGTCTCCCAAAACA 1500
QY 1501 GCAAGCGCTGGAAGAGAAAGAGATTACACTTCCCAAGCTACCTGGAATAGCCAT 1560
DB 1501 GCAAGCGCTGGAAGAGAAAGAGATTACACTTCCCAAGCTACCTGGAATAGCCAT 1560
QY 1561 TTACTGCAATAGGAGTCTTCTTAATGCTGTATGAGTGAACATCTGTGCGGAAT 1620
DB 1561 TTACTGCAATAGGAGTCTTCTTAATGCTGTATGAGTGAACATCTGTGCGGAAT 1620
QY 1621 GAAAGACAGACCAAGAAACAGACTTCAGACGACGCGGTGTGCAAACTGACCAA 1680
DB 1621 GAAAGACAGACCAAGAAACAGACTTCAGACGACGCGGTGTGCAAACTGACCAA 1680
QY 1681 AGGTATCCCTCTGCGGAGACAGGTAAACATTTGCGTGAATCAAGTGAATGCTC 1740
DB 1681 AGGTATCCCTCTGCGGAGACAGGTAAACATTTGCGTGAATCAAGTGAATGCTC 1740
QY 1741 CAAACACCGGCTGAGAGATTAACAACAGCCTCTTCAACGGGAGACCAACCCCATGCT 1800
DB 1741 CAAACACCGGCTGAGAGATTAACAACAGCCTCTTCAACGGGAGACCAACCCCATGCT 1800
QY 1801 GGCAGGGGTCTCCAGATATGAATTCAGAGAACCCAAATGGAGTTTCAAGAGATTA 1860
DB 1801 GGCAGGGGTCTCCAGATATGAATTCAGAGAACCCAAATGGAGTTTCAAGAGATTA 1860
QY 1861 GCTGACACTGGGCAAGCCCTGAGAGAAAGTTTGTGGCAAGTGTATATGGCGGAAC 1920
DB 1861 GCTGACACTGGGCAAGCCCTGAGAGAAAGTTTGTGGCAAGTGTATATGGCGGAAC 1920
QY 1921 AGTGGAAATTGAACAAGACCAAGCCAAAGAGGCGGTCACTGTGCGGTGAAGATGTTGAA 1980

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Db      1921  AGTGGGATTTGACAAAGACCAAGCCCAAGAGGCGGTCAACCTGGCCGTGGAAGATGTTGAA 1980
Qy      1981  AGATGATGCCACAGAGAAAGACCTTTCTGATCTGGTGTGAGAGATGAGATGATGAAGAT 2040
Db      1981  AGATGATGCCACAGAGAAAGACCTTTCTGATCTGGTGTGAGAGATGAGATGATGAAGAT 2040
Qy      2041  GATTGGGAAACAAAGAAATATCATTAATCTTCTTGAGCCCTGCAACACAGATGGGCTCT 2100
Db      2041  GATTGGGAAACAAAGAAATATCATTAATCTTCTTGAGCCCTGCAACACAGATGGGCTCT 2100
Qy      2101  CTATGTCATAGTATGATAGTATGCTCTAAAGGCAACCTCCGAGAAATCTCCAGCCCGAG 2160
Db      2101  CTATGTCATAGTATGATAGTATGCTCTAAAGGCAACCTCCGAGAAATCTCCAGCCCGAG 2160
Qy      2161  GCCACCCGGGAGTAGTACTCTTAATGACATTAACCGTGTCTCTGAGAGACGATGACCTT 2220
Db      2161  GCCACCCGGGAGTAGTACTCTTAATGACATTAACCGTGTCTCTGAGAGACGATGACCTT 2220
Qy      2221  CAAGGACTTGGTGTATGACACCTTACAGCTGGCCAGACGAGTAGAGATCTTGGCTTCCCA 2280
Db      2221  CAAGGACTTGGTGTATGACACCTTACAGCTGGCCAGACGAGTAGAGATCTTGGCTTCCCA 2280
Qy      2281  AAAATGATTCATGAGATTTAGCAGCCAGAAATGTTTGGTAAACAGAAACATGTGAT 2340
Db      2281  AAAATGATTCATGAGATTTAGCAGCCAGAAATGTTTGGTAAACAGAAACATGTGAT 2340
Qy      2341  GAAAAATGACAGACTTTGAGACTCGCAGAGATATCAACATATGACATTAACAAAAAGAC 2400
Db      2341  GAAAAATGACAGACTTTGAGACTCGCAGAGATATCAACATATGACATTAACAAAAAGAC 2400
Qy      2401  CACCAATGGGGGGCTTCCAGTCAAGTGAATGGCTCCAGAAACCTGTGTTGATAGATATA 2460
Db      2401  CACCAATGGGGGGCTTCCAGTCAAGTGAATGGCTCCAGAAACCTGTGTTGATAGATATA 2460
Qy      2461  CACTCATCAGAGTATGTCTGTGCTTGGGGGTGTTAATGAGGAGATCTTCACTTAGG 2520
Db      2461  CACTCATCAGAGTATGTCTGTGCTTGGGGGTGTTAATGAGGAGATCTTCACTTAGG 2520
Qy      2461  CACTCATCAGAGTATGTCTGTGCTTGGGGGTGTTAATGAGGAGATCTTCACTTAGG 2520
Db      2461  CACTCATCAGAGTATGTCTGTGCTTGGGGGTGTTAATGAGGAGATCTTCACTTAGG 2520
Qy      2521  GGGGCTCGCCCTACCCAGGAGATCCCGTAGAGAACTTTTAAAGTGTCTGAAGAGACA 2580
Db      2521  GGGGCTCGCCCTACCCAGGAGATCCCGTAGAGAACTTTTAAAGTGTCTGAAGAGACA 2580
Qy      2581  CAGAAATGATAGCCAGGCACTGCAACCAAGAACTGTACATGATGAGAGGACTGTG 2640
Db      2581  CAGAAATGATAGCCAGGCACTGCAACCAAGAACTGTACATGATGAGAGGACTGTG 2640
Qy      2641  GCATGAGTGGCCCTCCAGAGACCAAGCTTCAAGCAAGTGTAGAGAACTTGGATCGAAT 2700
Db      2641  GCATGAGTGGCCCTCCAGAGACCAAGCTTCAAGCAAGTGTAGAGAACTTGGATCGAAT 2700
Qy      2701  TCTCACTCTCAACAACAATGAGAAATCTTGAACCTTCAAGCCACTCTCGAAGCAATATC 2760
Db      2701  TCTCACTCTCAACAACAATGAGAAATCTTGAACCTTCAAGCCACTCTCGAAGCAATATC 2760
Qy      2761  ACCATGTTACCTCTCAACAACAAGTCTTGTCTTCAGAGAAATATCTGTTTTTCTCC 2820
Db      2761  ACCATGTTACCTCTCAACAACAAGTCTTGTCTTCAGAGAAATATCTGTTTTTCTCC 2820
Qy      2821  AGACCCCATGCTTACGAAACCATGCTTCTCAAGTATCAACATTAACGGCAGTGTAA 2880
Db      2821  AGACCCCATGCTTACGAAACCATGCTTCTCAAGTATCAACATTAACGGCAGTGTAA 2880
Qy      2881  AACATGATGACTGTGTCTGCTGTGCTCCCAACAGAGACAGACTGGGAACTTAACAC 2940
Db      2881  AACATGATGACTGTGTCTGCTGTGCTCCCAACAGAGACAGACTGGGAACTTAACAC 2940
Qy      2941  TGACAGAGGAGAACATGCTTCCAGAGCTTGTGTCTTCACTTGTATATATGATCAGAG 3000
Db      2941  TGACAGAGGAGAACATGCTTCCAGAGCTTGTGTCTTCACTTGTATATATGATCAGAG 3000
Qy      3001  GAGTAAATTAATGAGAAAGTATACGATATGTGTAAAGATTTATACAGTTGAAACCTTG 3060

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Db      3001  GAGTAAATTAATGAGAAAGTATACGATATGTGTAAAGATTTATACAGTTGAAACCTTG 3060
Qy      3061  TAATCTTCCCAAGAGAGAAAGGTTTTTGTGAGACAGTGAATGTC 3106
Db      3061  TAATCTTCCCAAGAGAGAAAGGTTTTTGTGAGACAGTGAATGTC 3106
Qy      3061  TAATCTTCCCAAGAGAGAAAGGTTTTTGTGAGACAGTGAATGTC 3106

RESULT 2
ADZ13046
ID ADZ13046 standard; cDNA; 4612 BP.
XX
XX ADZ13046;
AC
XX
XX 16-JUN-2005 (first entry)
DT
XX
XX Human cancer-associated cDNA #164.
DE
XX
XX Diagnosis; DNA microarray; microarray; biochip; cancer; neoplasm;
KM
XX Cytosolic; gene; 88.
OS
XX Homo sapiens.
XX
XX NC02005031001-A2.
PN
XX
XX 07-APR-2005.
PD
XX
XX 23-SEP-2004; 2004MO-US031617.
PF
XX
XX 23-SEP-2003; 2003US-00669920.
PR
XX
XX (CHIR ) CHIRON CORP.
PA
XX
XX Morris DW, Malandro MS;
PI
XX
XX WPI; 2005-273395/28.
DR
XX
XX P-PSDB; ADZ13047.
DR
XX
XX
PT Nucleic acid array useful for detecting cancer associated nucleic acid,
PT comprises two or more nucleic acid probes.
XX
XX
XX Disclosure; SEQ ID NO 566; 198bp; English.
XX
XX
XX The invention relates to a nucleic acid array for detecting a cancer
XX associated (CA) nucleic acid, comprising two or more nucleic acid probes.
XX The invention also relates to a peptide array comprising two or more
XX isolated polypeptides encoded by a CA nucleic acid sequence, a compound
XX that binds to a polypeptide, an isolated antibody or its fragment which
XX binds to a polypeptide, which is prepared by immunizing a host animal
XX with a composition comprising the polypeptide or its antigen binding
XX fragment and collecting cells from the host expressing antibodies against
XX the antigen or its antigen binding fragment, a composition comprising the
XX antibody and a carrier, a method of screening for anticancer activity, a
XX method of detecting a CA nucleic acid, a method of diagnosing cancer, a
XX method of treating cancer and a method of inhibiting expression of a CA
XX nucleic acid in a cell. The CA nucleic acids are useful for detecting CA
XX nucleic acids. The antibody is useful for detecting the presence or
XX absence of cancer cells in an individual which involves contacting cells
XX from the individual with the antibody and detecting a complex of a CA
XX protein from the cancer cells and the antibody, where the detection of
XX the complex correlates with the presence of cancer cells in the
XX individual. The composition is useful for inhibiting growth of cancer
XX cells in an individual or for delivering a therapeutic agent to cancer
XX cells in an individual. The invention is also useful for diagnosing
XX cancer, for treating cancer and for inhibiting expression of a CA gene in
XX a cell. This sequence represents human cancer-associated cDNA of the
XX invention.

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SQ Sequence 4612 BP; 1238 A; 1090 C; 1165 G; 1119 T; 0 U; 0 Other;
Query Match 97.4%; Score 3025.4; DB 14; Length 4612;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 3100; Conservative 0; Mismatches 6; Indels 11; Gaps 6;

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QY 1 CCCGCGAGCAAAAGTTGTTGTTGAGAGCAACG-CAAGCTGAGTCTTCTTCTCTGTTCC 59
DB 187 CTCGCGAGCAAAAGTTGTTGTTGAGAGCAACGCAAGCTGAGTCTTCTTCTCTCTGTTCC 246
QY 60 CCAAAATCCGAGGGCAACCCCGGGCGGTCAATG---GGGCTCTCCGAGCGTGGGGATACCG 116
DB 247 CCAAAATCCGAGGGCAACCCCGGGCGGTCAATG---GGGCTCTCCGAGCGTGGGGATACCG 306
QY 117 GTGAAGCCCGAGGAGGCTTGGCGCCGGCGAAGACCAAGAGCACTCTCTGCGTTTGAG 176
DB 307 GTGAAGCCCGAGGAGGCTTGGCGCCGGCGAAGACCAAGAGCACTCTCTGCGTTTGAG 366
QY 177 TTGCTCCCCGCAACCCCGGGCTGTGCTTCTTCCATCCCGACCCAGCGGGGC-CGGG 235
DB 367 TTGCTCCCCCAACCCCGGGCTGTGCTTCTTCCATCCCGACCCAGCGGGGC-CGGG 426
QY 236 ACAACACAGGTGCGCGAGAGGCGTTGCAATGAGGAGCTGCGAGCGAGCG-CCAGCGCC 294
DB 427 ACAACACAGGTGCGCGAGAGGCGTTGCAATGAGGAGCTGCGAGCGAGCG-CCAGCGCC 486
QY 295 TCGGTTCTTGAGGCCCAACCGCA-CCGTAAGGCAATTGCGCGTATGCAATGCGCGTATGAGAA 353
DB 487 TCGGTTCTTGAGGCCCAACCGCAAGCGCTGAAAGCAATTGCGCGTATGCAATGCGCGTATGAGAA 546
QY 354 GTGTGCAAGTGGATTTAACTTCAATGAGATATGAGAGAGACCGGGGATTTGGTACCG 413
DB 547 GTGTGCAAGTGGATTTAACTTCAATGAGATATGAGAGAGACCGGGGATTTGGTACCG 606
QY 414 TAAACATGTCACGTGGGGGTGTTTCACTGCGCGGTGCGTGCACCATGGGCAACTTGT 473
DB 607 TAAACATGTCACGTGGGGGTGTTTCACTGCGCGGTGCGTGCACCATGGGCAACTTGT 666
QY 474 CCGTGGCCCGGCGCTCTTCAAGTTAAGTTAGAGATACCACTTAAAGCCAAAGAGCAC 533
DB 667 CCGTGGCCCGGCGCTCTTCAAGTTAAGTTAGAGATACCACTTAAAGCCAAAGAGCAC 726
QY 534 CAACCAAAATACCAAAATCTTCAACAGAGATGTAAGTGGCGCCAGGGGAAATCGGTAG 593
DB 727 CAACCAAAATACCAAAATCTTCAACAGAGATGTAAGTGGCGCCAGGGGAAATCGGTAG 786
QY 594 AGGTGCGCTGCGTGTGTAAGATGCGCGCGTATCAATTGAGACTTAAAGATGGGGTGCAT 653
DB 787 AGGTGCGCTGCGTGTGTAAGATGCGCGCGTATCAATTGAGACTTAAAGATGGGGTGCAT 846
QY 654 TGGGGCCCAACAATAGAGCAGTGTATTGAGGAGTACTTGACAGATTAAGCGGCCAC 713
DB 847 TGGGGCCCAACAATAGAGCAGTGTATTGAGGAGTACTTGACAGATTAAGCGGCCAC 906
QY 714 CTAGAGACTCGGCTCTATGCTTGTATCTGCGAGTATGAGACTGTGAAAGCTTGGT 773
DB 907 CTAGAGACTCGGCTCTATGCTTGTATCTGCGAGTATGAGACTGTGAAAGCTTGGT 966
QY 774 ACTTCAGTGAATGTCACAGATGCGCATCTCATCCGAGATGATGAGATGACCGATG 833
DB 967 ACTTCAGTGAATGTCACAGATGCGCATCTCATCCGAGATGATGAGATGACCGATG 1026
QY 834 GTGCGAAGAAATTTGTGTCAGTGAAGACGTAAACAACAAGAGCACTACTGTGACCAACA 893
DB 1027 GTGCGAAGAAATTTGTGTCAGTGAAGACGTAAACAACAAGAGCACTACTGTGACCAACA 1086
QY 894 CAGAAAAGATGGAAGAGCGGCTCATGCTGTGCGCGCCMACATGTCAGATTTGGCT 953
DB 1087 CAGAAAAGATGGAAGAGCGGCTCATGCTGTGCGCGCCMACATGTCAGATTTGGCT 1146
QY 954 GCCCAGCGGGGGGAAACCAATGCAACAATGCGGTGCTGAAAAACGGGAGGAGTTTA 1013
DB 1147 GCCCAGCGGGGGGAAACCAATGCAACAATGCGGTGCTGAAAAACGGGAGGAGTTTA 1206
QY 1014 AGCAGAGCATGCGATTGAGAGCTTACAGAGTACGAAACCAAGCACTGAGGCTCTATTATGG 1073
DB 1207 AGCAGAGCATGCGATTGAGAGCTTACAGAGTACGAAACCAAGCACTGAGGCTCTATTATGG 1266
QY 1074 AAAGTGTGTCCATCTGACAGAGGAAATTAATACCTGTGTATGTGAGAAATGAAATACGGGT 1133

DB 1267 AAAGTGTGTCCATCTGACAAAGGAAATTAATACCTGTGTGTGTGAGAAATGAAATACGGGT 1326
QY 1134 CCATCAATCAACAGTATACCACTGATGTTGTGAGACGATGCGCTCAACGGGCCATCTTCC 1193
DB 1327 CCATCAATCAACAGTATACCACTGATGTTGTGAGACGATGCGCTCAACGGGCCATCTTCC 1386
QY 1194 AAGCGGACTGCGGGCAAAATGCTTCAAGATGTGTGAGAGAGACCTAAGTTTGTCTCA 1253
DB 1387 AAGCGGACTGCGGGCAAAATGCTTCAAGATGTGTGAGAGAGACCTAAGTTTGTCTCA 1446
QY 1254 AGTTTAAAGTATGCCAGCCCAATCCAGTGTATCAAGACCTGTGAAAAAGACGGCA 1313
DB 1447 AGTTTAAAGTATGCCAGCCCAATCCAGTGTATCAAGACCTGTGAAAAAGACGGCA 1506
QY 1314 GTTAAATACGGGCGCAACGGGCTGCTTCAAGATTTCTCAAGCACTCGGGGATTAATA 1373
DB 1507 GTTAAATACGGGCGCAACGGGCTGCTTCAAGATTTCTCAAGCACTCGGGGATTAATA 1566
QY 1374 GTTCCAAATGCAAGATGCTGCTTCTTCAATGTGACCGAAGCGGATGCTGGGAAATATA 1433
DB 1567 GTTCCAAATGCAAGATGCTGCTTCTTCAATGTGACCGAAGCGGATGCTGGGAAATATA 1626
QY 1434 TATGTAAAGTCTCAATTATATAGGACAGGCAACAGTCTGCTGACTGCTTGC 1493
DB 1627 TATGTAAAGTCTCAATTATATAGGACAGGCAACAGTCTGCTGACTGCTTGC 1686
QY 1494 CAAAAACAGACGCGCTGAGAGAAAGAGATTAACAGTCTTCCCAAGCTACCTGAGAGA 1553
DB 1687 CAAAAACAGACGCGCTGAGAGAAAGAGATTAACAGTCTTCCCAAGCTACCTGAGAGA 1746
QY 1554 TAGCCATTTATCTGCAATAGGGGCTTCTTAAATGCGCGTATGAGTGAACAGTATCTGT 1613
DB 1747 TAGCCATTTATCTGCAATAGGGGCTTCTTAAATGCGCGTATGAGTGAACAGTATCTGT 1806
QY 1614 GCGGAATGAAGAAACAGACCAAGAAAGCAGACTTACAGACCGCGCTGTGCAAAAC 1673
DB 1807 GCGGAATGAAGAAACAGACCAAGAAAGCAGACTTACAGACCGCGCTGTGCAAAAC 1866
QY 1674 TGAACAAAGTATCCCTCTGCGAGACAGTAAAC---AGTTTGGCTGATGTCAGCTTC 1729
DB 1867 TGAACAAAGTATCCCTCTGCGAGACAGTAAAC---AGTTTGGCTGATGTCAGCTTC 1926
QY 1730 TCCATGAATCTCAACACCGCGCTGTGAGAGATTAACAACGCGCTCTTCAACGGCAGAC 1789
DB 1927 TCCATGAATCTCAACACCGCGCTGTGAGAGATTAACAACGCGCTCTTCAACGGCAGAC 1986
QY 1790 ACCCCATGCTGGCAGGGGCTTCCGAGTATGAACCTTCCAGAGGACCCAAATGGAGTTT 1849
DB 1987 ACCCCATGCTGGCAGGGGCTTCCGAGTATGAACCTTCCAGAGGACCCAAATGGAGTTT 2046
QY 1850 CCAAGAGATAGCTGACACTGGGCAAGCCCTTGGGAGAAAGTTTGGCTTGGCAAGTGTTC 1909
DB 2047 CCAAGAGATAGCTGACACTGGGCAAGCCCTTGGGAGAAAGTTTGGCTTGGCAAGTGTTC 2106
QY 1910 ATGCGCGAAGCAGTGGGAATTTGACAAAGCAAGCCCAAGAGCGGTGACCGTGGCCGTG 1969
DB 2107 ATGCGCGAAGCAGTGGGAATTTGACAAAGCAAGCCCAAGAGCGGTGACCGTGGCCGTG 2166
QY 1970 AAGATGTTGAAGATGATGCTCACAGAGAAAGACCTTTCGATCTGTGTCAAGATGAGAG 2029
DB 2167 AAGATGTTGAAGATGATGCTCACAGAGAAAGACCTTTCGATCTGTGTCAAGATGAGAG 2226
QY 2030 ATGATGAAGATGATGAGGAAACCAAGAAATATCATTAATCTTCTTGGAGCTGACACAG 2089
DB 2227 ATGATGAAGATGATGAGGAAACCAAGAAATATCATTAATCTTCTTGGAGCTGACACAG 2286
QY 2090 GATGGGCTCTCTATATCTCATATGTTGATAGTGTCTTAAAGGCAACTCCGAGAAATACCTC 2149
DB 2287 GATGGGCTCTCTATATCTCATATGTTGATAGTGTCTTAAAGGCAACTCCGAGAAATACCTC 2346
QY 2150 CGAGCCCGAGGCGCAACCGGGATGAGTACTCTATGACATTTAACCGTGTCTCTGAGAG 2209

Db	2347	CGAGCCGGAGGCCACCCGGGATGAGATCTCTATGACATTTAAACCGTGTCTCGAGAG	2406
Qy	2210	CAGATGACCTTCAAGAGCTTGSTGTCAATGACCTACACAGCTGGCCAGACGGATGAGATAC	2269
Db	2407	CAGATGACCTTCAAGGACTTGSTGTCAATGACCTACACAGCTGGCCAGAGGCAATGAGTAC	2466
Qy	2270	TTGGCTTCCCAAAATGTATTCATCTGAGATTTAGCAGCCAGAAATGTTTTGGTAAACGAA	2329
Db	2467	TTGGCTTCCCAAAATGTATTCATGAGATTTAGCAGCCAGAAATGTTTTGGTAAACGAA	2526
Qy	2330	AACAATGATGAAAAATAGCAGCTTTGGACTGCGCAGAGATCAACAATATATGACAT	2389
Db	2527	AACAATGATGAAAAATAGCAGCTTTGGACTGCGCAGAGATCAACAATATATGACAT	2586
Qy	2450	GATAGAGTATACACTCATCAGATGATGTCTGTGCTCTTGGGGTGTATATGTGGAGATC	2509
Db	2647	GATAGAGTATACACTCATCAGATGATGTCTGTGCTCTTGGGGTGTATATGTGGAGATC	2706
Qy	2510	TTCACTTTAGGGGGGTGGCCTTACCCAGAGGATCCCGGAGGAACTTTTTAACTGTGT	2559
Db	2707	TTCACTTTAGGGGGGTGGCCTTACCCAGAGGATCCCGGAGGAACTTTTTAACTGTGT	2766
Qy	2570	AAGGAAGGACACAGATATGATATAGCAGCCCAACTGACCAACGAATCTGTATCATGATG	2629
Db	2767	AAGGAAGGACACAGATATGATATAGCAGCCCAACTGACCAACGAATCTGTATCATGATG	2826
Qy	2630	AGGGACTGTGGCATGCAATGAGTCCCTCCCAAGAGACCAACGTTCAAGCAATGTGTAAAGAC	2689
Db	2827	AGGGACTGTGGCATGCAATGAGTCCCTCCCAAGAGACCAACGTTCAAGCAATGTGTAAAGAC	2886
Qy	2680	TTGGATCGAATTTCTCACTCTCAACAACAAATAGGAATTTCTTGACCTCAGCCAACCTCTC	2749
Db	2887	TTGGATCGAATTTCTCACTCTCAACAACAAATAGGAATTTCTTGACCTCAGCCAACCTCTC	2946
Qy	2750	GAAACGATTTACCTAGTTAACCTCGTACACAAGAAAGTTCTTGTCTTTCAGAGATGATCT	2809
Db	2947	GAAACGATTTACCTAGTTAACCTCGTACACAAGAAAGTTCTTGTCTTTCAGAGATGATCT	3006
Qy	2810	GTTTTTTTCTCAGACCCCGATGCTTTCGAGACATGCTCTCTCAGATCCACATTAAC	2869
Db	3007	GTTTTTTTCTCAGACCCCGATGCTTTCGAGACATGCTCTCTCAGATCCACATTAAC	3066
Qy	2870	GGCAGTGTAAACATGATATGATCTGTCTGCTCTGTCCCAACAGGACAGCATCTGGGA	2929
Db	3067	GGCAGTGTAAACATGATATGATCTGTCTGCTCTGTCCCAACAGGACAGCATCTGGGA	3126
Qy	2930	CCTGAGTACACTGAGCAGGAGAACCATGCTCCCAAGAGCTGTGTCTCCACTGTATAT	2989
Db	3127	CCTGAGTACACTGAGCAGGAGAACCATGCTCCCAAGAGCTGTGTCTCCACTGTATAT	3186
Qy	2990	ATGATCATGAGAGATTAATTAATTTGGAAAAATATCAGATATGTGTAAAGATTTATACG	3049
Db	3187	ATGATCATGAGAGATTAATTAATTTGGAAAAATATCAGATATGTGTAAAGATTTATACG	3246
Qy	3050	TTGAAAACTTGTATCTTCCCGAGAGGAGAAAGGTTTCTGAGCATGTGACTGC	3106
Db	3247	TTGAAAACTTGTATCTTCCCGAGAGGAGAAAGGTTTCTGAGCATGTGACTGC	3303
RESULT 3			
ADZ13092			
ID ADZ13052 standard; cDNA, 5003 BP.			
ADZ13052;			
AC			
XX ADZ13052;			
XX			
DT 16-JUN-2005 (first entry)			
XX Human cancer-associated cDNA #167.			
XX			

XX	Diagnosis; DNA microarray; microarray; biochip; cancer; neoplasia;
XX	Cytostatic; gene; 88.
XX	Homo sapiens.
XX	MO2005031001-A2.
XX	07-APR-2005.
XX	23-SEP-2004; 2004WO-US031617.
XX	23-SEP-2003; 2003US-00669920.
XX	(CHIR) CHIRON CORP.
XX	Morris DW, Malandro MS;
XX	WPI: 2005-273395/28.
XX	P-PSDB; ADZ13053.
XX	Nucleic acid array useful for detecting cancer associated nucleic acid,
XX	comprises two or more nucleic acid probes.
XX	Disclosure; SEQ ID NO 572; 198pp; English.
XX	The invention relates to a nucleic acid array for detecting a cancer
XX	associated (CA) nucleic acid, comprising two or more nucleic acid probes.
XX	The invention also relates to a peptide array comprising two or more
XX	isolated polypeptides encoded by a CA nucleic acid sequence, a compound
XX	that binds to a polypeptide, an isolated antibody or its fragment which
XX	binds to a polypeptide, which is prepared by immunizing a host animal
XX	with a composition comprising the polypeptide or its antigen binding
XX	fragment and collecting cells from the host expressing antibodies against
XX	the antigen or its antigen binding fragment, a composition comprising the
XX	antibody and a carrier, a method of screening for anticancer activity, a
XX	method of detecting a CA nucleic acid, a method of diagnosing cancer, a
XX	method of treating cancer and a method of inhibiting expression of a CA
XX	nucleic acid in a cell. The CA nucleic acids are useful for detecting CA
XX	nucleic acids. The antibody is useful for detecting the presence or
XX	absence of cancer cells in an individual which involves contacting cells
XX	from the individual with the antibody and detecting a complex of a CA
XX	protein from the cancer cells and the antibody, where the detection of
XX	the complex correlates with the presence of cancer cells in the
XX	individual. The composition is useful for inhibiting growth of cancer
XX	cells in an individual or for delivering a therapeutic agent to cancer
XX	cells in an individual. The invention is also useful for diagnosing
XX	cancer, for treating cancer and for inhibiting expression of a CA gene in
XX	a cell. This sequence represents human cancer-associated cDNA of the
XX	invention.
XX	Sequence 5003 BP; 1330 A; 1189 C; 1260 G; 1224 T; 0 U; 0 Other;
XX	Query Match 97.4%; Score 3025.4; DB 14; Length 5003;
XX	Best Local Similarity 99.5%; Pred. No. 0;
XX	Matches 3100; Conservative 0; Mismatches 6; Indels 11; Gaps 6;
XX	1 CCGGAGCAAGTTGGTGGAGGCAAG-CAAGCTGAGTCTTTCTCTCTGTTCC 59
XX	578 CTCGGAGCAAGTTGGTGGAGGCAAGCCAGAGCTGAGTCTTTCTCTCTGTTCC 637
XX	60 CCAATCCGAGGGAGGCCCGCGGGCGTCAAT--GCGCTCTCTCCGACGCTGGGGTACGC 116
XX	Db CCAATCCGAGGGAGGCCCGCGGGCGTCAATCCGCGCTCTCTCCGACGCTGGGGTACGC 697
XX	117 GTGAAGCCCGGAGGCTTGGGCGGCGGGAAGACCAAGAGACACTCTTGGGTTGGAG 176
XX	Db GTGAAGCCCGGAGGCTTGGGCGGCGGGAAGACCAAGAGACACTCTTGGGTTGGAG 757
XX	177 TTGCTCCCGGCAACCCGCGGGCTCGTCTCTTCATCCGAGCCACGCGGGGC-CGGGG 235
XX	Db TTGCTCCCGGCAACCCGCGGGCTCGTCTCTTCATCCGAGCCACGCGGGGC-CGGGG 817
XX	236 ACAACACAGAGTCCGGAGAGAGCGTTTGCCATTCAAGTGAATCGACAGCAGC-GCAGCGCC 294

Db	818	ACAAACAAGGTCGGGAGAGACGTTGGCATTCAAGTACATGCAAGCAAGCCAGCGCC	877
OY	295	TCGGTCTCTGAGCCCAACCGCA-GCTGAAGCATTCGCCGTAGTCAATGCCCCGTAGAGAA	353
Db	878	TCGGTCTCTGAGCCCAACCGCAAGCTGAAGGATTCGCCGTAGTCAATGCCCCGTAGAGAA	937
OY	354	GTGTGCAGATGGGATTAACTGTCAATGAGATATGAAAGGACCGGGATTGGTACCG	413
Db	928	GTGTGCAGATGGGATTAACTGTCAATGAGATATGAAAGGACCGGGATTGGTACCG	997
OY	414	TAACTATGTCAGCTGGGGTGGTTTATCTGCGCGGTGTGATCAATGGCAACTGTG	473
Db	998	TAACTATGTCAGCTGGGGTGGTTTATCTGCGCGGTGTGATCAATGGCAACTGTG	1057
OY	474	CCCTGAGCCGAGCCCTCTTCAGTTTAGTTGAGATACCACTTAGACCCAGAGACCA	533
Db	1058	CCCTGAGCCGAGCCCTCTTCAGTTTAGTTGAGATACCACTTAGACCCAGAGACCA	1117
OY	534	CAACCAATATCCAAATCTCTCAACGAGATGTACGTGGCTGCGCAGGGAGTCGTAG	593
Db	1118	CAACCAATATCCAAATCTCTCAACGAGATGTACGTGGCTGCGCAGGGAGTCGTAG	1177
OY	594	AGGTGCGCTGCTGTTGAAAGATGCCCCGCGATCAGTTGACCTAAAGATTCGGGTGACT	653
Db	1178	AGGTGCGCTGCTGTTGAAAGATGCCCCGCGATCAGTTGACCTAAAGATTCGGGTGACT	1237
OY	654	TGGGCCCCAACAATAGGACAGTGTCTTATGGGGAGTACTTSCAATTAAGGCGCCACAC	713
Db	1238	TGGGCCCCAACAATAGGACAGTGTCTTATGGGGAGTACTTSCAATTAAGGCGCCACAC	1297
OY	714	CTAGAAGCTCCGGCCTCTATGCTGTGACTGCGCAGTAGGACTGTAGACGTGAACCTTGGT	773
Db	1298	CTAGAAGCTCCGGCCTCTATGCTGTGACTGCGCAGTAGGACTGTGAACCTTGGT	1357
OY	774	ACTTCATGTGATGTGCAGATGCGATCTCATCCGAGATGATGAGGATGACCGATG	833
Db	1358	ACTTCATGTGATGTGCAGATGCGATCTCATCCGAGATGATGAGGATGACCGATG	1417
OY	834	GTGGCGAAGATTTTGTGCAGTGAAGACAGTAAACAACAAGAGCACCATCTGACCAACA	893
Db	1418	GTGGCGAAGATTTTGTGCAGTGAAGACAGTAAACAACAAGAGCACCATCTGACCAACA	1477
OY	894	CAGAAAAGATGAAAAAGCGGCTCATGCTGTGCTCGCGCCACACTGTCAAGTTTGGCT	953
Db	1478	CAGAAAAGATGAAAAAGCGGCTCATGCTGTGCTCGCGCCACACTGTCAAGTTTGGCT	1537
OY	954	GCCCCAGCCGGGGGAAACCTAATGCCAACTATGCCATCATTCGGGTGAGAAAAACGGGAAGGATTTA	1013
Db	1538	GCCCCAGCCGGGGGAAACCTAATGCCAACTATGCCATCATTCGGGTGAGAAAAACGGGAAGGATTTA	1597
OY	1014	AGCAGAGATGAGCATTTGAGAGCTTCAAGGTACGAAACACAGACTGAGAGCTCTATTATG	1073
Db	1598	AGCAGAGATGAGCATTTGAGAGCTTCAAGGTACGAAACACAGACTGAGAGCTCTATTATG	1657
OY	1074	AAAGTGTGTCCATCTGACAAAGGAAATTATCTGTGTAGTGAAGATGAATACGGGT	1133
Db	1658	AAAGTGTGTCCATCTGACAAAGGAAATTATCTGTGTAGTGAAGATGAATACGGGT	1717
OY	1134	CCATCATCAACACGTACCACTTGATGTTGTGAGCGATCGCTCAACGGGCCATCTCC	1193
Db	1718	CCATCATCAACACGTACCACTTGATGTTGTGAGCGATCGCTCAACGGGCCATCTCC	1777
OY	1194	AAAGCCGACCTGCCGGAATNGCTCCACAGTGTGGAGAGACGTAGAGTTTGTCTGCA	1253
Db	1778	AAAGCCGACCTGCCGGAATNGCTCCACAGTGTGGAGAGACGTAGAGTTTGTCTGCA	1837
OY	1254	AGGTTTACAGTATGCCAGCCCAACATCAAGTATCAAGACGTGAAAAAGAACCGCA	1313
Db	1838	AGGTTTACAGTATGCCAGCCCAACATCAAGTATCAAGACGTGAAAAAGAACCGCA	1897
OY	1314	GTAAATTCAGGACCGGCTGCTTACCTCAAGTTTCAAGCACTTCGGGATTAATA	1373

Db	1898	GTAATAAGCGGCCGACGAGCGGCTGCCCTCACTCAAGGTTCTCAAGCACTCGGAGGATTAATA	1957
Qy	1314	GTTCCAAATGCAAGAAAGTGCTGGCTCTGTTTCAATGACCCGAGCGGAGATGCTGGGGAAATATA	1433
Db	1958	GTTCCAAATGCAAGAAAGTGCTGGCTCTGTTTCAATGACCCGAGCGGAGATGCTGGGGAAATATA	2017
Qy	1434	TATGTAAAGTCTCCAAATTAATATAGGAGGACCAACAGTCTGGCTGACTCATGTCCTGC	1493
Db	2018	TATGTAGGTCTCCAAATTAATATAGGAGGACCAACAGTCTGGCTGACTCATGTCCTGC	2077
Qy	1494	CAAAAACAGCAAGCGCTGGAAAGAAAAAGAGATTACAGCTTCCCCAGACTACTGAGAGA	1553
Db	2078	CAAAAACAGCAAGCGCTGGAAAGAAAAAGAGATTACAGCTTCCCCAGACTACTGAGAGA	2137
Qy	1554	TAGCAATTACTGCA TAGGGGTCTTTTAAACGCGCTGATAGGTAGTTAAAGTCACTACCTGT	1613
Db	2138	TAGCAATTACTGCA TAGGGGTCTTTTAAACGCGCTGATAGGTAGTTAAAGTCACTACCTGT	2197
Qy	1614	GCCGAATGAAGAACAGACCAAGAAAGCCAGACTTCAGACGACCAACCGGCTGTGACAAAGC	1673
Db	2198	GCCGAATGAAGAACAGACCAAGAAAGCCAGACTTCAGACGACCAACCGGCTGTGACAAAGC	2257
Qy	1674	TGACCAAAAGTATCCCCCTGCGGAGACAGGTAC---AGTTTGCGCTGATCCAGCTCC	1729
Db	2258	TGACCAAAAGTATCCCCCTGCGGAGACAGGTATACAGAAAGTTTGGGCTGATCCAGCTCC	2317
Qy	1730	TTCATGAATCCCAACACCCCGCTGGTAGATTAACAACGCGCTCTCTTCAACGGGACAC	1789
Db	2318	TTCATGAATCCCAACACCCCGCTGGTAGATTAACAACGCGCTCTCTTCAACGGGACAC	2377
Qy	1790	ACCCCAATGCTGGCAGGGGTCTCCAGATATACTTCAGAGAGACCCAAATGAGAGTTT	1849
Db	2378	ACCCCAATGCTGGCAGGGGTCTCCAGATATACTTCAGAGAGACCCAAATGAGAGTTT	2437
Qy	1850	CCAAAGATTAAGCTGACACTGCGCAAGCCCTGCGAGAAAGTTGCTTTGGCAAGTGTCT	1909
Db	2438	CCAAAGATTAAGCTGACACTGCGCAAGCCCTGCGAGAAAGTTGCTTTGGGCAAGTGTCT	2497
Qy	1910	ATGGCGGAAGCAGTGGGAATTGACAAACAAGCCCAAGAGGGGGTCAACGCTGGCCGTG	1969
Db	2498	ATGGCGGAAGCAGTGGGAATTGACAAACAAGCCCAAGAGGGGGTCAACGCTGGCCGTG	2555
Qy	1970	AAGATGTTGAAGATGATGCGCACAGAGAAAGACTTTTCTGATCTGCTGTCTCAGAGATGAG	2029
Db	2558	AAGATGTTGAAGATGATGCGCACAGAGAAAGACTTTTCTGATCTGCTGTCTCAGAGATGAG	2617
Qy	2030	ATGATGAAGATGTTGGGAAACAAGAATATCATTAATCTTTCTTGAAGCTGCACACAG	2088
Db	2618	ATGATGAAGATGTTGGGAAACAAGAATATCATTAATCTTTCTTGAAGCTGCACACAG	2677
Qy	2090	GATGGGCTCTCTATGTCTCATAGTTAGATAGTGCCTTAAAGGCAACCTCCAGAAATACCTC	2144
Db	2678	GATGGGCTCTCTATGTCTCATAGTTAGATAGTGCCTTAAAGGCAACCTCCAGAAATACCTC	2733
Qy	2150	CGAGCCCGGAGGCAACCGGGATGGAGTACTCTCTATGAACATTAACCGTGTCTGAGAG	2205
Db	2738	CGAGCCCGGAGGCAACCGGGATGGAGTACTCTCTATGAACATTAACCGTGTCTGAGAG	2797
Qy	2210	CAGATGACCTTCAAGACTTGTGTCTATGCACTCAACAGCTGGCCAGACGAGTGAATAC	2265
Db	2798	CAGATGACCTTCAAGACTTGTGTCTATGCACTCAACAGCTGGCCAGAGCAATGAGTAC	2855
Qy	2270	TTGGCTTCCCAAAATGTATTCATGAGATTAGCAGCCCAAGAAATGTTTGGTAAACAGAA	2322
Db	2858	TTGGCTTCCCAAAATGTATTCATGAGATTAGCAGCCCAAGAAATGTTTGGTAAACAGAA	2917
Qy	2330	AAACAATGATGAATAATAGCAACTTTGGAACCTCGCAGAGATATCAACAATATTAAGTAT	2385
Db	2918	AAACAATGATGAATAATAGCAACTTTGGAACCTCGCAGAGATATCAACAATATTAAGTAT	2977
Qy	2390	TACAAAAGACCAACCAATGGGCGGCTTCCAGTCAAGTGAATGGCTTCCAGAACCCCTGTTT	2445
Db	2978	TACAAAAGACCAACCAATGGGCGGCTTCCAGTCAAGTGAATGGCTTCCAGAACCCCTGTTT	3033

QY	2450	GATTAAGATATACATCAATCAAGAGTATGTCTGCTTCGGGGGTGTTAATGCGGAATC	2509
Db	3038	GATAGATATATACATCAATCAAGATATGTCTGCTTCGGGGGTGTTAATGCGGAATC	3097
QY	2510	TTCACTTTAGGGGGCTCGCCCTACCCAGGGAATCCCGTGAGAACTTTTAAAGCTCGT	2569
Db	3098	TTCACTTTAGGGGGCTCGCCCTACCCAGGGAATCCCGTGAGAACTTTTAAAGCTCGT	3157
QY	2570	AAGGAAGGACACAGAATGATTAAGCAGCCAACTGCACCAAGAGACTGTACATGATGATG	2629
Db	3158	AAGGAAGGACACAGAATGATTAAGCAGCCAACTGCACCAAGACTGTACATGATGATG	3217
QY	2630	AGGACTGTGGCATGACAGTGCCTCTCCAGAGACCAAGCTTCAAGCACTTGATGATGAAG	2689
Db	3218	AGGACTGTGGCATGACAGTGCCTCTCCAGAGACCAAGCTTCAAGCACTTGATGATGAAG	3277
QY	2630	TTGATCGAATTTCTCACTCTCAACAACATAGAGAAATCTTGACCTCAGCCAACTCTC	2749
Db	3278	TTGATCGAATTTCTCACTCTCAACAACATAGAGAAATCTTGACCTCAGCCAACTCTC	3337
QY	2750	GAACTGATTTCACTCAATTTACCTCTCAACAAGAACTTGTCTTCAGAGATGATCT	2809
Db	3338	GAACTGATTTCACTCAATTTACCTCTCAACAAGAACTTGTCTTCAGAGATGATCT	3397
QY	2810	GTTTTTTCTCGAAGCCCATGCTTACGAACCATGCTTCTCTCAATATCCACATAAAC	2869
Db	3398	GTTTTTTCTCGAAGCCCATGCTTACGAACCATGCTTCTCTCAATATCCACATAAAC	3457
QY	2870	GGCACTGTTAAAAATGAAATGAATCTGTGTCTGCTCTCTCCCAACAGACACTGGGAA	2929
Db	3458	GGCACTGTTAAAAATGAAATGAATCTGTGTCTGCTCTCTCCCAACAGACACTGGGAA	3517
QY	2930	CCTAGCTTCACTGACAGGAGAACCATGCTCCCGAGACTGTGTCTCCACTTGTATAT	2989
Db	3518	CCTAGCTTCACTGACAGGAGAACCATGCTCCCGAGACTGTGTCTCTCCACTTGTATAT	3577
QY	2990	ATGATCAAGAGAGTAAATTAATTGAAAAAGTATCATGATATGTGTAAAGATTTATACAG	3049
Db	3578	ATGATCAAGAGAGTAAATTAATTGAAAAAGTATCATGATATGTGTAAAGATTTATACAG	3637
QY	3050	TTGAAAACCTGTAAATCTTCCCGAGAGAGAAAGGTTTCTGAGACATGACCTGC	3106
Db	3638	TTGAAAACCTGTAAATCTTCCCGAGAGAGAAAGGTTTCTGAGACATGACCTGC	3694

XX	RESULT 4
XX	ADL61208
XX	ID ADL61208 standard; DNA; 4574 BP.
XX	ADL61208;
XX	03-JUN-2004 (first entry)
XX	Human tyrosine kinase biomarker fibroblast growth factor receptor 2 DNA
XX	predictor set; protein tyrosine kinase; cyrostatic; antiangiogenic;
KW	vasotrophic; vlnary; pharmacogenomic; drug sensitivity; breast cancer
KW	hypervascular disease; angiogenesis; wound healing scar; human;
XX	biomarker; de; gene; fibroblast growth factor receptor 2.
XX	Homo sapiens.
-OS	
PN	WO2004020583-A2.
XX	
PD	11-MAR-2004.
XX	
PF	26-AUG-2003; 2003WO-US026491.
XX	
PR	27-AUG-2002; 2002US-0406385P.
XX	
PA	(BRIM) BRISTOL-MYERS SQUIBB CO.
XX	

PI	Huang F, ¹ Han X, ¹ Reeves KA, ¹ Amlier L, ¹ Fairchild CR, ¹ Lee FY,
Pt	Shaw P;
XX	
DR	wpi ¹ ; 2004-239171/22.
DR	P-PSDB; AD161330.
XX	
PT	New predictor sets with a plurality of polynucleotides and/or
PT	polypeptides whose expression pattern predicts cell response to a
PT	compound that modulates protein tyrosine kinase activity, useful in
PT	treating breast cancer.
XX	
XX	Claim 2; SEQ ID NO 132; 649bp; English.
CC	
CC	The invention relates to a novel predictor set comprising a plurality of
CC	polynucleotides and/or polypeptides whose expression pattern is
CC	predictive of the response of cells to treatment with a compound that
CC	modulates protein tyrosine kinase activity or members of the protein
CC	tyrosine kinase pathway. The molecules of the invention demonstrate
CC	cytostatic, antiangiogenic, vasotropic and vulnerary activities and may
CC	be useful in the field of pharmacogenomics, in particular for determining
CC	drug sensitivity and in treating breast cancer. Hypervascular diseases, of
CC	angiogenesis and scars in wound healing. The current sequence is that of
CC	a human protein tyrosine kinase biomarker DNA of the invention.
XX	
SQ	Sequence 4574 BP; 1231 A; 1085 C; 1149 G; 1109 T; 0 U; 0 Other;
Query Match	97.0%; Score 3013.2; DB 12; Length 4574;
Best Local Similarity	99.5%; Pred. No. 0;
Matches 3097; Conservative	0; Mismatches 8; Indels 9; Gaps 7
QY	1 CCCGCGAGCAAAAGTTTGTGGAGGCAACG -CAACCCTGAATCCTTTCTTCCTCTCCGTTCC 59
DG	
DG	168 CTCGCAGCAAAAGTTTGTGGAGGCAACGCCAACCTGAATCCTTTCTTCCTCTCCGTTCC 227
QY	60 CCAAAATCCGAGGGACGCCGCGGGGCGTATG---GCGCTCCTCCGACGACTGGGGATAACG 116
DG	
DG	228 CCAAAATCCGA-GGCAACCCCGCGGGGCGTATGCCCCGCTCTCTCGCACGCTGGGGGTAACG 286
QY	117 G-TGAAGCCCGGGAGGCTTGCGCGCGCGAAGAACCAGACAATTCTGCGTTTGA 175
DG	
DG	287 GCGAAAGCCCGGGAGGCTTGCGCGCGCGAAGACCAAGAGCACTCTTCGCGTTTGA 346
QY	176 GTTGCTCCCCGCAACCCCGGGGCTGTCGCTTTCATCCCGAACCAAGCGGGGCG-CGGG 224
DG	
DG	347 GTTGCTCCCCCAAAACCCCGGGGCTGTCGCTTTCATCCCGAACCCAGCCGCGGGCGCGGG 406
QY	235 GACAAACACAGTCGCGGAGAGACGTTGCGCATTCAGAGTACGTGACAGACGACG--GCAAGCG 293
DG	
DG	407 GACAAACACAGTCGCGGAGAGACGTTGCGCATTCAGAGTACGTGACAGACGACGCGACGCG 466
QY	294 CTGCGTCTCTGAGGCCACCGCA-GCTGAAGGCATTGGCGGTAGTCATGCCCCTTAGAGA 352
DG	
DG	467 CTGCGTCTCTGAGGCCACCGCAAGGTGAAGGCATTGGCGGTAGTCATGCCCCTTAGAGA 526
QY	353 AGTGTGACAGTGGATTTAAAGTCCATGACATGAGATATGAAAGAGACCGGGGAAATTGGTACC 412
DG	
DG	527 AGTGTGACAGTGGATTTAAAGTCCATGACATGAGATATGAAAGAGACCGGGGAAATTGGTACC 586
QY	413 GTAACCAATGATGATGCGGGGTCGTTTCAATCTGCGTGTGCGGTGACCAATGGCAACCTTG 472
DG	
DG	587 GTAACCAATGATGATGCGGGGTCGTTTCAATCTGCGTGTGCGGTGACCAATGGCAACCTTG 646
QY	473 TTCCTGAGCCGGGCGCTCCTCTCAAGTTTAGTTAGATACCAATTAGAGCCAGAAAGACCA 532
DG	
DG	647 TTCCTGAGCCGGGCGCTCCTCTCAAGTTTAGTTAGATACCAATTAGAGCCAGAAAGACCA 706
QY	533 CCAACCAAATACCAAAATCTTCAACACAGAGTGTACGTGCGCGCAAGGGGAGTGGCTTA 592
DG	
DG	707 CCAACCAAATACCAAAATCTTCAACACAGAGTGTACGTGCGCGCAAGGGGAGTGGCTTA 766
QY	593 GAGGTGCGCTGCTGTGTAAAAGATGCGCCGCTGATCAAGTTGACATTAAGATATGGGGTGAC 652
DG	
DG	767 GAGGTGCGCTGCTGTGTAAAAGATGCGCCGCTGATCAAGTTGACATTAAGATATGGGGTGAC 826

QY	653	TTGGGGCCCAACAATAGACA	GTGCTATT	TTGGGGAGTACTT	CGATTAAGGCCCA	CA	712
Db	827	TTGGGGCCCAACAATAGACA	GTGCTATT	TTGGGGAGTACTT	CGATTAAGGCCCA	CG	886
QY	713	CCTAGACATCCGGGCTCTA	TGCTTGA	CTGCGCAGT	GTAGCTGTAG	CAAGTAACTTGG	772
Db	887	CCTAGACATCCGGGCTCTA	TGCTTGA	CTGCGCAGT	GTAGCTGTAG	CAAGTAACTTGG	946
QY	773	TACTTCATGTGAATGTCA	CAGATGCCATCT	CA	TCGGAGTATGATGAC	CA	832
Db	947	TACTTCATGTGAATGTCA	CAGATGCCATCT	CA	TCGGAGTATGATGAC	CA	1006
QY	833	GGTGGGAAGATTTTGTG	CATGTAGAA	CA	GTAA	CA	892
Db	1007	GGTGGGAAGATTTTGTG	CATGTAGAA	CA	GTAA	CA	1066
QY	893	ACAGAAAAGATGAAAAAG	CGGCTCA	TGCTGTG	CTGCGGCA	CA	952
Db	1067	ACAGAAAAGATGAAAAAG	CGGCTCA	TGCTGTG	CTGCGGCA	CA	1126
QY	953	TGCCCAGCGGGGGGAA	CCCAATG	CCAA	CCATGCGGTG	CTGAAAA	1012
Db	1127	TGCCCAGCGGGGGGAA	CCCAATG	CCAA	CCATGCGGTG	CTGAAAA	1186
QY	1013	AAGCAGAGCATCGATTG	GAGGCTA	CA	AGGTAC	GA	1072
Db	1187	AAGCAGAGCATCGATTG	GAGGCTA	CA	AGGTAC	GA	1246
QY	1073	GAAATGTGTCCCATCTG	ACAAGGAA	TTAT	CTGTGATG	GGAA	1132
Db	1247	GAAATGTGTCCCATCTG	ACAAGGAA	TTAT	CTGTGATG	GGAA	1306
QY	1133	TCCATCAATCA	CA	CGTAC	CA	CGTGA	1192
Db	1307	TCCATCAATCA	CA	CGTAC	CA	CGTGA	1366
QY	1193	CAAGCCGGA	CTGCGCGGA	TA	TGCTT	CA	1252
Db	1367	CAAGCCGGA	CTGCGCGGA	TA	TGCTT	CA	1426
QY	1253	AAGTTTACAGTATGCC	ATGCCCCA	CA	TCCAGT	GGATCA	1312
Db	1427	AAGTTTACAGTATGCC	ATGCCCCA	CA	TCCAGT	GGATCA	1486
QY	1313	AGTAAATACGGGCGCG	ACGAGGCT	CA	AGTCT	CA	1372
Db	1487	AGTAAATACGGGCGCG	ACGAGGCT	CA	AGTCT	CA	1546
QY	1373	AGTTCCATG	CAGAA	GTGTG	CTGT	CA	1432
Db	1547	AGTTCCATG	CAGAA	GTGTG	CTGT	CA	1606
QY	1433	ATATGTAA	GGTCCCA	TTAT	T	AGGG	1492
Db	1607	ATATGTAA	GGTCCCA	TTAT	T	AGGG	1666
QY	1493	CCAAAACACAGCGCTG	GAAGAGAA	AGAA	AGATTA	CAG	1552
Db	1667	CCAAAACACAGCGCTG	GAAGAGAA	AGAA	AGATTA	CAG	1726
QY	1553	ATAGCATT	TACTG	CA	TAGGGG	CTTCTT	1612
Db	1727	ATAGCATT	TACTG	CA	TAGGGG	CTTCTT	1786
QY	1613	TGCGGATGA	GAAC	CGAC	CA	AA	1672
Db	1787	TGCGGATGA	GAAC	CGAC	CA	AA	1846
QY	1673	CTGAC	CCAA	CGTAT	CCCCCT	GTGGG	1732
Db	1847	CTGAC	CCAA	CGTAT	CCCCCT	GTGGG	1906

QY	1733	ATGAAGCTCCAA	CA	CCCCGCTGGTGGAGATTA	CA	CA	CGCTCTCTTCA	ACGGCAG	CACC	1792											
Db	1907	ATGAAGCTCCAA	CA	CCCCGCTGGTGGAGATTA	CA	CA	CGCTCTCTTCA	ACGGCAG	CACC	1966											
QY	1793	CCCATGCTGGCA	GGGGGTCTCCGAGTAT	GA	CA	CTTCCAGAGGACCCAA	AAATGGGAG	TTTCCA		1852											
Db	1967	CCCATGCTGGCA	GGGGGTCTCCGAGTAT	GA	CA	CTTCCAGAGGACCCAA	AAATGGGAG	TTTCCA		2026											
QY	1853	AGAGATTAAGCT	GACACTGGGCA	AGCCCCCTGGGAGAA	GGTGTCTTTGGGCA	AGTGTG	CTATG			1912											
Db	2027	AGAGATTAAGCT	GACACTGGGCA	AGCCCCCTGGGAGAA	GGTGTCTTTGGGCA	AGTGTG	CTATG			2086											
QY	1913	GCGGAAGCAGT	GGGAAATTGCA	AAAGAC	CA	AGCCCCAGAGGCGGTCA	CCCTGGCCCTG	GAAG		1972											
Db	2087	GCGGAAGCAGT	GGGAAATTGCA	AAAGAC	CA	AGCCCCAGAGGCGGTCA	CCCTGGCCCTG	GAAG		2146											
QY	1973	ATGTTGAAAGT	GTATGTCACAG	AAAGAC	CCTTCTGATCTGGGTG	TCAGAGATG	AGAGATG			2032											
Db	2147	ATGTTGAAAGT	GTATGTCACAG	AAAGAC	CCTTCTGATCTGGGTG	TCAGAGATG	AGAGATG			2206											
QY	2033	ATGAAGATGAT	TGGGAAAC	CA	CA	AAAGATATCA	TAAATCTTGGAG	CGCTG	CA	CA	AGAT	2092									
Db	2207	ATGAAGATGAT	TGGGAAAC	CA	CA	AAAGATATCA	TAAATCTTGGAG	CGCTG	CA	CA	AGAT	2266									
QY	2093	GGGCGCTCTA	TATGTCATATG	TGAGTATG	CGCTTAA	AGCA	CA	CTCCGAGAA	ATCCTCCG			2152									
Db	2267	GGGCGCTCTA	TATGTCATATG	TGAGTATG	CGCTTAA	AGCA	CA	CTCCGAGAA	ATCCTCCG			2326									
QY	2153	GGCCGGAAGG	CCACCCGGGATGG	AGATATCCTCTA	AGATTA	CA	ATTAACG	GTGTTCTG	AGAGAG	CAG		2212									
Db	2327	GGCCGGAAGG	CCACCCGGGATGG	AGATATCCTCTA	AGATTA	CA	ATTAACG	GTGTTCTG	AGAGAG	CAG		2386									
QY	2213	ATGACCTTCA	AGAGCTTGGTGTCA	TGTGCA	TGCA	CTTAC	CTTAC	CGTGGC	CAGA	CGGATG	AGATCTTG	2272									
Db	2387	ATGACCTTCA	AGAGCTTGGTGTCA	TGTGCA	TGCA	CTTAC	CTTAC	CGTGGC	CAGA	CGGATG	AGATCTTG	2446									
QY	2273	GCTTCCAAAA	AAATGTATTCAT	CGAGATTTAG	ACAGCCAG	GA	AAATGTTTGGT	ATTA	CGGAGAA	C		2332									
Db	2447	GCTTCCAAAA	AAATGTATTCAT	CGAGATTTAG	ACAGCCAG	GA	AAATGTTTGGT	ATTA	CGGAGAA	C		2506									
QY	2333	AATGTGATG	AAATATG	CGACCTTTG	AGATG	CGCAGAG	ATATCA	CAATATATG	ATGATTA	C		2392									
Db	2507	AATGTGATG	AAATATG	CGACCTTTG	AGATG	CGCAGAG	ATATCA	CAATATATG	ATGATTA	C		2566									
QY	2393	AAAAAGAC	CA	CA	CAATGGGCGGCTT	CA	CA	CTCAAGT	GGATG	CGTCCAG	AAAGCCCTG	TTTGAT	2452								
Db	2567	AAAAAGAC	CA	CA	CAATGGGCGGCTT	CA	CA	CTCAAGT	GGATG	CGTCCAG	AAAGCCCTG	TTTGAT	2626								
QY	2453	AGAGTATAC	CTCAT	CA	AGTATG	TATGTCTGTG	CTCTTCCGGG	GGTTAA	ATGTGG	GA	AT	CTTC	2512								
Db	2627	AGAGTATAC	CTCAT	CA	AGTATG	TATGTCTGTG	CTCTTCCGGG	GGTTAA	ATGTGG	GA	AT	CTTC	2686								
QY	2513	ACTTTAAGGG	GGGTGCGCCCTAC	CA	AGGAA	TTCCG	GTGAGAA	CA	CTTTTAA	AC	CT	CTG	AA	2572							
Db	2687	ACTTTAAGGG	GGGTGCGCCCTAC	CA	AGGAA	TTCCG	GTGAGAA	CA	CTTTTAA	AC	CT	CTG	AA	2746							
QY	2573	GAAAGCA	CAG	AATG	AGATTA	AGCCAG	CA	CA	CTGCA	CA	CA	AGATG	ATG	AG	2632						
Db	2747	GAAAGCA	CAG	AATG	AGATTA	AGCCAG	CA	CA	CTGCA	CA	CA	AGATG	ATG	AG	2806						
QY	2633	GACTGTGG	CATG	CAG	TGCGCTTCC	CA	AGAC	CA	AGTTC	CA	AG	CA	G	AGT	AG	2692					
Db	2807	GACTGTGG	CATG	CAG	TGCGCTTCC	CA	AGAC	CA	AGTTC	CA	AG	CA	G	AGT	AG	2866					
QY	2693	GATCGA	ATTC	ATC	ATCTCA	CA	AGCA	CA	ATG	AGAA	ATCTT	GG	AG	CA	CT	CG	AA	2752			
Db	2867	GATCGA	ATTC	ATC	ATCTCA	CA	AGCA	CA	ATG	AGAA	ATCTT	GG	AG	CA	CT	CG	AA	2926			
QY	2753	CAGTATTC	AC	CTA	AGTTAC	CC	CTG	AC	CA	AA	AG	ATCTT	GT	CTT	CA	GA	AG	AT	CT	GT	2812
Db	2927	CAGTATTC	AC	CTA	AGTTAC	CC	CTG	AC	CA	AA	AG	ATCTT	GT	CTT	CA	GA	AG	AT	CT	GT	

Db 2987 TTTTCTCCAGACCCCATGCTTACGAAACATGCTCTCTCAGATCCACATTAACGGC 3046
 Qy 2873 AGTGTAAACATGAATGACTGTGTCTGCTGTCTCCCAACAGAGACGACTGGAACTT 2932
 Db 3047 AGTGTAAACATGAATGACTGTGTCTGCTGTCTCCCAACAGAGACGACTGGAACTT 3106
 Qy 2933 AGTCACTAGACGAGGAGACATGCTCTCCAGAGCTTGTGTCTCCACTTGTATATATG 2992
 Db 3107 AGCTACACTGAGACGAGACATGCTCTCCAGAGCTTGTGTCTCCACTTGTATATATG 3166
 Qy 2993 GATCAGAGAGTAATTAATTTGAAAAAGTAATCAGCATATGTATTAAGATTATACAGTTG 3052
 Db 3167 GATCAGAGAGTAATTAATTTGAAAAAGTAATCAGCATATGTATTAAGATTATACAGTTG 3226
 Qy 3053 AAAACTTGTATCTTCTCCAGAGAGAGAGAGGTTTCTGAGCAGTGAAGCTGC 3106
 Db 3227 AAACTGTATCTTCTCCAGAGAGAGAGAGGTTTCTGAGCAGTGAAGCTGC 3280
 RESULT 5
 ID ADQ80247 standard; cDNA; 4574 BP.
 AC ADQ80247;
 XX 21-OCT-2004 (first entry)
 DT 21-OCT-2004 (first entry)
 XX
 DE Fibroblast growth factor receptor 2 cDNA.
 XX
 KW bs; gene; cytosolic; epidermal growth factor receptor modulator;
 KM identification; therapeutic response; cancer; EGFR; biomarker.
 XX
 OS Homo sapiens.
 XX
 PN NO2004063709-A2.
 XX 29-JUL-2004.
 PD 08-JAN-2004; 2004MO-US000368.
 PF 08-JAN-2004; 2004US-0438735P.
 PR 08-JAN-2003; 2003US-0438735P.
 XX
 PA (BRIM) BRISTOL-MYERS SQUIBB CO.
 XX
 PI Amherst, January 1;
 XX
 DR WPI: 2004-544114/52.
 DR P-PSDB; ADQ80367.
 XX
 PT Identifying a mammal that will respond therapeutically to a method of
 PT treating cancer comprises comparing the level of a biomarker in a mammal
 PT before and after exposure to an epidermal growth factor receptor (EGFR)
 PT modulator.
 XX
 PS Disclosure; SEQ ID NO 19; 520bp; English.
 PS
 XX
 CC The invention relates to a method of identifying a mammal that will
 CC respond therapeutically to a method of treating cancer by administering
 CC an epidermal growth factor receptor (EGFR) modulator by comparing the
 CC level of a biomarker in a mammal before and after exposure to an EGFR
 CC modulator. The method comprises: (a) measuring, in the mammal, the level
 CC of at least one biomarker identified in the specification; (b) exposing
 CC the mammal to the EGFR modulator; and (c) measuring in the mammal the
 CC level of the biomarker, where a difference in the level in step (c)
 CC compared to step (a) indicates that the mammal will respond
 CC therapeutically to the method of treating cancer. The method and
 CC biomarkers are useful for identifying a mammal that will respond
 CC therapeutically to a method of treating cancer by administering an
 CC epidermal growth factor receptor (EGFR) modulator. This sequence
 CC corresponds to one of the biomarkers whose levels of gene expression is
 CC measured in the method of the invention.
 CC
 XX

SQ Sequence 4574 BP; 1231 A; 1085 C; 1149 G; 1109 T; 0 U; 0 Other;
 Query Match 97.0%; Score 3013.2; DB 13; Length 4574;
 Best Local Similarity 99.5%; Pred. No. 0;
 Matches 3097; Conservative 0; Mismatches 8; Indels 9; Gaps 7;
 Qy 1 CCCGAGCAAAAGTTGTTGAGAGCAACG-CAAGCTGAATCTTCTCTCTGTTCC 59
 Db 168 CTGCGAGAAAGTTTGTGAGAGGACCAAGCTGATCTTCTCTCTGTTCC 227
 Qy 60 CCAATCCAGAGGCGAGCGCGCGGTCAATG--GCGTCTCTCCGAGCTGGGTACCG 116
 Db 228 CCAATCCGA-GGCAGCGCGCGCGGTCAATGCGCGCTCTCTCCGAGCTGGGTACCG 286
 Qy 117 G-TGAAGCCCGGAGGCTTGGCGCGGAGAGCCCAAGACCAACTCTCTGCTTGA 175
 Db 287 GCTGAAGCCCGGAGGCTTGGCGCGGAGAGCCCAAGACCAACTCTCTGCTTGA 346
 Qy 176 GTTGCTCCCGCAACCCCGGCTCGTCTCTCTCTCTCCATCCGACCGCGGCGC-CGGG 234
 Db 347 GTTGCTCCCGCAACCCCGGCTCGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 406
 Qy 235 GACCAACAGAGTCCGAGAGAGGCTTCCATTCAGTGAATGCTGAGCAGCAGC-GCAGCGC 293
 Db 407 GACCAACAGAGTCCGAGAGAGGCTTCCATTCAGTGAATGCTGAGCAGCAGCAGCGC 466
 Qy 294 CTGCTCTCTGAGCCCAACCGCA-GCTGAAGGCAATGCGGCTAGTCATGCGCTAGAGA 352
 Db 467 CTGCTCTCTGAGCCCAACCGCAAGGCTGAAGGCAATGCGGCTAGTCATGCGCTAGAGA 526
 Qy 353 AGTGTGAGAGGAGATTAAGTCAATGAGATATGAGAGAGACCGGAGATTGTATAC 412
 Db 527 AGTGTGAGAGGAGATTAAGTCAATGAGATATGAGAGAGACCGGAGATTGTATAC 586
 Qy 413 GTAACATGATGACTGAGGAGTCTTCAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 472
 Db 587 GTAACATGATGACTGAGGAGTCTTCAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 646
 Qy 473 TCCCTGCGCGCGCT 532
 Db 647 TCCCTGCGCGCGCT 706
 Qy 533 CCAACCAATACCAATCTCTCAACAGAGATGATGATGATGATGATGATGATGATGATGAT 592
 Db 707 CCAACCAATACCAATCTCTCAACAGAGATGATGATGATGATGATGATGATGATGATGAT 766
 Qy 593 GAGTGCCTGCTCTGTTGAAGATGCGCGGTGATGATGATGATGATGATGATGATGATGAT 652
 Db 767 GAGTGCCTGCTCTGTTGAAGATGCGCGGTGATGATGATGATGATGATGATGATGATGAT 826
 Qy 653 TTGGGCGCCAAATGAGACATGCTTATTTGGGAGTACTTGCAGATTAAGGGCGCAC 712
 Db 827 TTGGGCGCCAAATGAGACATGCTTATTTGGGAGTACTTGCAGATTAAGGGCGCAC 886
 Qy 713 CTTAGAGACTCCGCGCTATGCTTATGCTGACAGTGAAGCTGTAAGAGTGAAGCTTGG 772
 Db 887 CTTAGAGACTCCGCGCTATGCTTATGCTGACAGTGAAGCTGTAAGAGTGAAGCTTGG 946
 Qy 773 TACTTATGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 832
 Db 947 TACTTATGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1006
 Qy 833 GGTGCGGAAGTTTGTGAGTGAAGACATGTAACAAGAGACACATCTGAGACCAAC 892
 Db 1007 GGTGCGGAAGTTTGTGAGTGAAGACATGTAACAAGAGACACATCTGAGACCAAC 1066
 Qy 893 ACAGAAAAGTGAAGAAAGGCGCTCAATGCTGCTGCGGCAACCTGCAAGTTTGG 952
 Db 1067 ACAGAAAAGTGAAGAAAGGCGCTCAATGCTGCTGCGGCAACCTGCAAGTTTGG 1126
 Qy 953 TGCCAGCGCGGAGAAACCAATGCAACCATGCGGTGCTGTAAGAAAGGAGATT 1012
 Db 1127 TGCCAGCGCGGAGAAACCAATGCAACCATGCGGTGCTGTAAGAAAGGAGATT 1186

QY 1013 AAGCAGAGCATCGCATTTGGAGGCTTCAAGATACGAACCAAGCTGAGGCTCATTTATG 1072
DB 1187 AAGCAGAGCATCGCATTTGGAGGCTTCAAGATACGAACCAAGCTGAGGCTCATTTATG 1246
QY 1073 GAAAGTGTGCTCCATCTGACAAAGGAAATTATCTGTGTAGTGGAGAAATGAATCGGG 1132
DB 1247 GAAAGTGTGCTCCATCTGACAAAGGAAATTATCTGTGTAGTGGAGAAATGAATCGGG 1306
QY 1133 TCCATCAATCAACGTAACCACTGATGTTGTGAGAGCATCGGCTGACCGGCCATCTTC 1192
DB 1307 TCCATCAATCAACGTAACCACTGATGTTGTGAGAGCATCGGCTGACCGGCCATCTTC 1366
QY 1193 CAAGCCGAGCTGCGGCAAAATGCTTCAAGTGTGAGAGAGCATGAAATTTGTCTGC 1252
DB 1367 CAAGCCGAGCTGCGGCAAAATGCTTCAAGTGTGAGAGAGCATGAAATTTGTCTGC 1426
QY 1253 AAGGTTTACAGTATGATCCAGCCCACTTCAGTGTGATCAAGCACTGGAGAAACGGC 1312
DB 1427 AAGGTTTACAGTATGATCCAGCCCACTTCAGTGTGATCAAGCACTGGAGAAACGGC 1486
QY 1313 AATTAATACGGGCGCCGACGGGCTGACCTTACCTCAAGGTTCTCAAGCACTGGAGATAAT 1372
DB 1487 AATTAATACGGGCGCCGACGGGCTGACCTTACCTCAAGGTTCTCAAGCACTGGAGATAAT 1546
QY 1373 AGTTCCAAATGACAGATGCTGCTGTTCATATGTGACCGAGCGGATGCTGGGAAATAT 1432
DB 1547 AGTTCCAAATGACAGATGCTGCTGTTCATATGTGACCGAGCGGATGCTGGGAAATAT 1606
QY 1433 AATTTGTAAGTCTCCCAATTATATAGGCAAGCCCAAGCTGCTGAGCTCACTGCTCG 1492
DB 1607 AATTTGTAAGTCTCCCAATTATATAGGCAAGCCCAAGCTGCTGAGCTCACTGCTCG 1666
QY 1493 CCAAAACAGCAAGCGCTGAGAAAGAAAGAGATTACAGCTTCCCAAGCTACCTGAG 1552
DB 1667 CCAAAACAGCAAGCGCTGAGAAAGAAAGAGATTACAGCTTCCCAAGCTACCTGAG 1726
QY 1553 ATAGCCATTACTGATAGGAGGCTCTTCTTAATGCTGTATGCTGTATACAGTATCTG 1612
DB 1727 ATAGCCATTACTGATAGGAGGCTCTTCTTAATGCTGTATGCTGTATACAGTATCTG 1786
QY 1613 TGCAGTAATGAAGAACAGAACCAAGAGCCAGCTTCAGCAGCAGCGCTGTGACAAAG 1672
DB 1787 TGCAGTAATGAAGAACAGAACCAAGAGCCAGCTTCAGCAGCAGCGCTGTGACAAAG 1846
QY 1673 CTGACCAAAAGCTATCCCTCTGCGGAGACAGGTAAAGATTTCGCTGAGTCAAGCTCTCC 1732
DB 1847 CTGACCAAAAGCTATCCCTCTGCGGAGACAGGTAAAGATTTCGCTGAGTCAAGCTCTCC 1906
QY 1733 ATGAATCTCAACACCCCGCTGTGTAGAGTAACAACGCTCTCTTCAACGGCAACACC 1792
DB 1907 ATGAATCTCAACACCCCGCTGTGTAGAGTAACAACGCTCTCTTCAACGGCAACACC 1966
QY 1793 CCCATGCTGGCAGGGGCTCTCCAGTATGAATCTTCAAGAGACCCAAATATGGAGTTTCCA 1852
DB 1967 CCCATGCTGGCAGGGGCTCTCCAGTATGAATCTTCAAGAGACCCAAATATGGAGTTTCCA 2026
QY 1853 AGAGATTAAGCTGACACTGAGGCAAGCCCTGAGAGAAAGTTGCTTTGGGCAAGTGTCTAG 1912
DB 2027 AGAGATTAAGCTGACACTGAGGCAAGCCCTGAGAGAAAGTTGCTTTGGGCAAGTGTCTAG 2086
QY 1913 GCGGAGACAGTGGGAATTGACAAAGACCAAGCCCAAGAGGCGGTCACTGTCGCTGTAAG 1972
DB 2087 GCGGAGACAGTGGGAATTGACAAAGACCAAGCCCAAGAGGCGGTCACTGTCGCTGTAAG 2146
QY 1973 ATGTTGAAGATGATGTCACAGAGAAAGACCTTTCTGATCTGAGTCAAGAGATGAGATG 2032
DB 2147 ATGTTGAAGATGATGTCACAGAGAAAGACCTTTCTGATCTGAGTCAAGAGATGAGATG 2206
QY 2033 ATGAAGATGATTTGGGAAACCAAGAAATATCATTAATCTTTGGAGCCTGACACAGAT 2092
DB 2207 ATGAAGATGATTTGGGAAACCAAGAAATATCATTAATCTTTGGAGCCTGACACAGAT 2266

QY 2093 GGGGCTCTATGATGATGTTGAGATAGCTCTTAAAGGCAACTCCGAAATACCTCCGA 2152
DB 2267 GGGGCTCTCTATGATGATGTTGAGATAGCTCTTAAAGGCAACTCCGAAATACCTCCGA 2326
QY 2153 GCCCGAGAGCCACCCGGATGAGATCTCTATGACATTTAACGCTGTTCTTGAGAGCAG 2212
DB 2327 GCCCGAGAGCCACCCGGATGAGATCTCTATGACATTTAACGCTGTTCTTGAGAGCAG 2386
QY 2213 ATGACCTTCAAGGACTTGGTGTATGACCTTACCCAGCTGGCCAGACCGATGGAATCTTG 2272
DB 2387 ATGACCTTCAAGGACTTGGTGTATGACCTTACCCAGCTGGCCAGACCGATGGAATCTTG 2446
QY 2273 GCTTCCCAAAATGATTCATGAGATTTAGACGCCAGAAATGTTTGTAAACAAAAC 2332
DB 2447 GCTTCCCAAAATGATTCATGAGATTTAGACGCCAGAAATGTTTGTAAACAAAAC 2506
QY 2333 AATGTATGAATAATAGCAGACTTTGGAAGCTGCGCAGAGATATCAACATATAGACTATTAC 2392
DB 2507 AATGTATGAATAATAGCAGACTTTGGAAGCTGCGCAGAGATATCAACATATAGACTATTAC 2566
QY 2393 AAAAAGACCAACATGAGGCGGCTTCCAGTCAAGTGAATGCTCCAGAAAGCCCTGTTGAT 2452
DB 2567 AAAAAGACCAACATGAGGCGGCTTCCAGTCAAGTGAATGCTCCAGAAAGCCCTGTTGAT 2626
QY 2453 AAGATATACACTCATCAGATGATGTCGTCTTCCGGGATGTTATATGAGAGATCTTC 2512
DB 2627 AAGATATACACTCATCAGATGATGTCGTCTTCCGGGATGTTATATGAGAGATCTTC 2686
QY 2513 ACTTTAGGGGCTGCGCCCTACCCAGAGATTTCCGTGAGAGAACTTTTAACTGCTGAG 2572
DB 2687 ACTTTAGGGGCTGCGCCCTACCCAGAGATTTCCGTGAGAGAACTTTTAACTGCTGAG 2746
QY 2573 GAAAGCACAGATGATTAAGCAGACCACTGACCAACAGAACTGTATGATGAGG 2632
DB 2747 GAAAGCACAGATGATTAAGCAGACCACTGACCAACAGAACTGTATGATGAGG 2806
QY 2633 GACTGTGAGCATGAGTGCCTTCCAGAGACCAAGTTCAAGCAGTGTGATGAGACTTG 2692
DB 2807 GACTGTGAGCATGAGTGCCTTCCAGAGACCAAGTTCAAGCAGTGTGATGAGACTTG 2866
QY 2753 CAGTATTCACCTTATGCTTCAACCAATGAGAAATCTTGAACCTGACCACTCTCGAA 2752
DB 2867 CAGTATTCACCTTATGCTTCAACCAATGAGAAATCTTGAACCTGACCACTCTCGAA 2926
QY 2927 CAGTATTCACCTTATGCTTCAACCAATGAGAAATCTTGAACCTGACCACTCTCGAA 2986
DB 2813 TTTTCTCCAGACCCCATGCTTACGAACCATGCTTCTCAGTATTCACACATTAACGGC 2872
QY 2987 TTTTCTCCAGACCCCATGCTTACGAACCATGCTTCTCAGTATTCACACATTAACGGC 3046
QY 2873 AGTGTAAACATGATGATGCTGTGCTGTCCCTGCCAAACAGAGACGACTGGGAACCT 2932
DB 3047 AGTGTAAACATGATGATGCTGTGCTGTCCCTGCCAAACAGAGACGACTGGGAACCT 3106
QY 2933 AGCTTACCTGAGCAGGAGAACCATGCTTCCAGAGCTTGTTCCTCACTGTATATATG 2992
DB 3107 AGCTTACCTGAGCAGGAGAACCATGCTTCCAGAGCTTGTTCCTCACTGTATATATG 3166
QY 2993 GATCAGAGAGTAAATATTTGGAAAGTATAGCATATGTGTAAAGATTTATACAGTTG 3052
DB 3167 GATCAGAGAGTAAATATTTGGAAAGTATAGCATATGTGTAAAGATTTATACAGTTG 3226
QY 3053 AAAACTTGTATCTTCCCAAGAGAGAAAGAGTTTCTGAGCAGTGAATGCTG 3106
DB 3227 AAAACTTGTATCTTCCCAAGAGAGAGAAAGAGTTTCTGAGCAGTGAATGCTG 3280

RESULT 6
ACF91631
ID ACF91631 standard; DNA; 4574 BP.
XX

Db 1427 AAGTTTACAGTATGATCCAGGCCCCACATCAGTGCATCAGCACTGAGAAAAGAACGCGC 1486
 Qy 1313 AGTAATATAGGGGCGGACGGGGCTGCGCTCTCTCAAGGTTCTCAAGCACTCGGGGATAAAT 1372
 Db 1487 AGTAATATAGGGGCGGACGGGGCTGCGCTCTCTCAAGGTTCTCAAGCACTCGGGGATAAAT 1546
 Qy 1373 AGTTCCAAATGCAAGAGTGTGCTGTCTTCAATGTGACCGAGGCGGATGTGGGAAATAT 1432
 Db 1547 AGTTCCAAATGCAAGAGTGTGCTGTCTTCAATGTGACCGAGGCGGATGTGGGAAATAT 1606
 Qy 1433 ATATGTAAAGTCTTCAATATATAGGGCAGGCCAACCAAGTCTGCTGCTCACTGTCTG 1492
 Db 1607 ATATGTAAAGTCTTCAATATATAGGGCAGGCCAACCAAGTCTGCTGCTCACTGTCTG 1666
 Qy 1493 CCAAAAACAGCAAGCGCTGGAGAGAAAAGAGATTACAGCTTCCCAAGCTACCTGAG 1552
 Db 1667 CCAAAAACAGCAAGCGCTGGAGAGAAAAGAGATTACAGCTTCCCAAGCTACCTGAG 1726
 Qy 1553 ATAGCAATTTACTGCATAGGGGCTCTTCTTAATCGCCTGTATGAGTGTAAACAGTCAATCTG 1612
 Db 1727 ATAGCAATTTACTGCATAGGGGCTCTTCTTAATCGCCTGTATGAGTGTAAACAGTCAATCTG 1786
 Qy 1613 TCCCGAATGAAGAACAGACCAAGAACCCAGACTTCAAGCAGCCAGCGGCTGTGCAAG 1672
 Db 1787 TCCCGAATGAAGAACAGACCAAGAACCCAGACTTCAAGCAGCCAGCGGCTGTGCAAG 1846
 Qy 1673 CTGACCAAAAGTATCCCGCTGCGGAGACAGGTAAACAGTTTGGCTGAGTCAAGCTCTG 1732
 Db 1847 CTGACCAAAAGTATCCCGCTGCGGAGACAGGTAAACAGTTTGGCTGAGTCAAGCTCTG 1906
 Qy 1733 ATGAATCTCAACACCCCGCTGTGTAGAGATTAACAACAGCCTCTTCTCAACGCGACACCC 1792
 Db 1907 ATGAATCTCAACACCCCGCTGTGTAGAGATTAACAACAGCCTCTTCTCAACGCGACACCC 1966
 Qy 1793 CCCATGTGCGCAGGGGCTCTCCAGATATGAATCTTCAAGAGACCCCAAAATGGAGTTTCCA 1852
 Db 1967 CCCATGTGCGCAGGGGCTCTCCAGATATGAATCTTCAAGAGACCCCAAAATGGAGTTTCCA 2026
 Qy 1853 AGAGATTAAGCTGACACTGAGGCAAGCCCTGGAGAAAGTTGCTTGGGCAAGTGTATG 1912
 Db 2027 AGAGATTAAGCTGACACTGAGGCAAGCCCTGGAGAAAGTTGCTTGGGCAAGTGTATG 2086
 Qy 2087 GCGGAGCAGTGGGAATTGACAAAGACAGCCCAAGGAGCGGTCAACCGTGGCGGTGAG 2146
 Db 1973 ATGTGAAAGATGATGCGCACAGAGAAAGACCTTCTGATCTGCTGTGAGATGAGATG 2032
 Qy 2147 ATGTGAAAGATGATGCGCACAGAGAAAGACCTTCTGATCTGCTGTGAGATGAGATG 2206
 Db 2033 ATGAAGATGATGGGGAACACAGAAATATCATTAATCTTCTGAGGCTGCAACAGAT 2092
 Qy 2207 ATGAAGATGATGGGGAACACAGAAATATCATTAATCTTCTGAGGCTGCAACAGAT 2266
 Db 2267 GGGGCTCTCATATGCTATAGTTAGTATGCTCTTAAGGCAACCTCCGAGAAATACCTCGA 2326
 Qy 2153 GCGCGGAGGCGACCCCGGATGAGATATCTCTATGACATTAACCGTGTCTTGGAGGACAG 2212
 Db 2327 GCGCGGAGGCGACCCCGGATGAGATATCTCTATGACATTAACCGTGTCTTGGAGGACAG 2386
 Qy 2213 ATGACCTTCAAGAGCTTGTGTGATGACCTACAGCTGCGCAGACGATGAGATGATG 2272
 Db 2387 ATGACCTTCAAGAGCTTGTGTGATGACCTACAGCTGCGCAGACGATGAGATGATG 2446
 Qy 2273 GCTTCCCAAAATATATTCATGAGATTAGACCCAGAAATGTTTTGTTAAAGAAAC 2332
 Db 2447 GCTTCCCAAAATATATTCATGAGATTAGACCCAGAAATGTTTTGTTAAAGAAAC 2506
 Qy 2333 AATGTGATGAATAATGACAGCTTTGAGTCCCGCAGAGATATCAACATATATGATATTAAC 2392

Db 2507 AATGTGATGAATAATGACAGCTTTGGAGCTCGCCAGAGATATCAACATATATGACTATTAC 2566
 Qy 2393 AAAAAACCAACCAATAGGGGCTTCCAGTCAAAGTGAATGCTCCGAAGACCTGTTTGAAT 2452
 Db 2567 AAAAAACCAACCAATAGGGGCTTCCAGTCAAAGTGAATGCTCCGAAGACCTGTTTGAAT 2626
 Qy 2453 AAGATATACATCAATCAGAGTGAATGCTGCTTCCGAGGAGTTAATGAGGAGATCTTC 2512
 Db 2627 AAGATATACATCAATCAGAGTGAATGCTGCTTCCGAGGAGTTAATGAGGAGATCTTC 2686
 Qy 2513 ACTTTAGGGGCTCGCCCTTACCAGAGATTCCTGTGAGAGAACTTTTAAGTGTGAG 2572
 Db 2687 ACTTTAGGGGCTCGCCCTTACCAGAGATTCCTGTGAGAGAACTTTTAAGTGTGAG 2746
 Qy 2573 GAAAGACACAGAAATGATAGCCAGCCAACTGACCAACAGAACTGTATCATATGATGAG 2632
 Db 2747 GAAAGACACAGAAATGATAGCCAGCCAACTGACCAACAGAACTGTATCATATGATGAG 2806
 Qy 2633 GACTGTGGCAGTACAGTGCCTCCAGAGACCAAGGTTCAAGCAGTGTAGAAAGCTTG 2692
 Db 2807 GACTGTGGCAGTACAGTGCCTCCAGAGACCAAGGTTCAAGCAGTGTAGAAAGCTTG 2866
 Qy 2693 GATCGAATTCCTCACTCTCAACCAATGAGAAATCTTGAACCTCAGCCAACTCTGAA 2752
 Db 2867 GATCGAATTCCTCACTCTCAACCAATGAGAAATCTTGAACCTCAGCCAACTCTGAA 2926
 Qy 2753 CAGTATTCACCTTATGTTACCTTGAACACAGAAAGTTCTTGTCTTCAAGAGATGATCTGTT 2812
 Db 2927 CAGTATTCACCTTATGTTACCTTGAACACAGAAAGTTCTTGTCTTCAAGAGATGATCTGTT 2986
 Qy 2813 TTTTTCGAGACCCCAATGCTTACAGAACCATGCTTCCAGATTCACACATTAACGCG 2872
 Db 2987 TTTTTCGAGACCCCAATGCTTACAGAACCATGCTTCCAGATTCACACATTAACGCG 3046
 Qy 2873 AGTGTAAACATGATGATGCTGTCTGCTGTCCGCAACAGACAGCACTGGGAACCT 2932
 Db 3047 AGTGTAAACATGATGATGCTGTCTGCTGTCCGCAACAGACAGCACTGGGAACCT 3106
 Qy 2933 AGTCACTGAGAGGAGACATGCTTCCAGAGCTTGTGTCTTCACTTGTATATG 2992
 Db 3107 AGTCACTGAGAGGAGACATGCTTCCAGAGCTTGTGTCTTCACTTGTATATG 3166
 Qy 2993 GATCAGAGAGTAAATTAATTTGAAAAGTATGACATATGTGTAAGATTATACAGTTG 3052
 Db 3167 GATCAGAGAGTAAATTAATTTGAAAAGTATGACATATGTGTAAGATTATACAGTTG 3226
 Qy 3053 AAAACTTGTATCTTCCCGAGAGAGAAAGTTTCTGAGCAGTGAATGC 3106
 Db 3227 AAAACTTGTATCTTCCCGAGAGAGAAAGTTTCTGAGCAGTGAATGC 3280

RESULT 7
 ID AEA81172 standard; DNA; 4574 BP.
 AEA81172;
 25-AUG-2005 (first entry)
 Human fibroblast growth factor receptor-2 transcript variant 2 DNA.
 screening; obesity; nutritional disorder; anorectic; db; gene;
 fibroblast growth factor receptor-2; FGF receptor-2; transcript variant.
 Homo sapiens.
 US2005136465-A1.
 23-JUN-2005.
 22-DEC-2004; 2004US-00019829.
 22-DEC-2003; 2003EP-00104902.

Db 1847 CTGACCAAAAGTATCCCTCCGCGAGACAGGTAAAGATTTCGGCTGAGTCCAGCTCTCC 1906
 Qy 1733 ATGAACTCCAAACACCCCGCTGTGTGAGATTAACAACACGCTCTTTCAACGCGACACCC 1792
 Db 1907 ATGAACTCCAAACACCCCGCTGTGTGAGATTAACAACACGCTCTTTCAACGCGACACCC 1966
 Qy 1793 CCCATCTGCGACAGGGGTCTCCGAGTATGAACCTTCCAGAGAACCCAAAATGGAGTTTCA 1852
 Db 1967 CCCATCTGCGACAGGGGTCTCCGAGTATGAACCTTCCAGAGAACCCAAAATGGAGTTTCA 2026
 Qy 1853 AGAGATTAAGCTGACACTGGGCAAGCCCTGGAGAAAGTTGCTTGGGCAAGTGTCAATG 1912
 Db 2027 AGAGATTAAGCTGACACTGGGCAAGCCCTGGAGAAAGTTGCTTGGGCAAGTGTCAATG 2086
 Qy 1913 GCGGAGACAGTGGGAAATTGACAAAGACAAAGCCCAAGAGCGGTCAACCTGCGCTGAAG 1972
 Db 2087 GCGGAGACAGTGGGAAATTGACAAAGACAAAGCCCAAGAGCGGTCAACCTGCGCTGAAG 2146
 Qy 1973 ATGTTGAAGATGATGCGACAGAGAAAGACCTTTGATCTGGTGTCAAGATGAGATG 2032
 Db 2147 ATGTTGAAGATGATGCGACAGAGAAAGACCTTTGATCTGGTGTCAAGATGAGATG 2206
 Qy 2033 ATGAAGATGATTGGGAAACACAGAAATATCATTAATCTTCTGAGGCTGACACAGAT 2092
 Db 2207 ATGAAGATGATTGGGAAACACAGAAATATCATTAATCTTCTGAGGCTGACACAGAT 2266
 Qy 2093 GGGCTCTCATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2152
 Db 2267 GGGCTCTCATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2326
 Qy 2153 GCGCGAGGCGCACCCCGGATGAGATGATGATGATGATGATGATGATGATGATGATGATG 2212
 Db 2327 GCGCGAGGCGCACCCCGGATGAGATGATGATGATGATGATGATGATGATGATGATGATG 2386
 Qy 2213 ATGACCTTCAAGGACTTGGTGTGATGATGATGATGATGATGATGATGATGATGATGATG 2272
 Db 2387 ATGACCTTCAAGGACTTGGTGTGATGATGATGATGATGATGATGATGATGATGATGATG 2446
 Qy 2273 GCTTCCCAAAATGATATTCATGAGATTTAGACGCGCAAAATGTTTGGTAAACAAAAAC 2332
 Db 2447 GCTTCCCAAAATGATATTCATGAGATTTAGACGCGCAAAATGTTTGGTAAACAAAAAC 2506
 Qy 2333 AATGTGATGAAATATGAGACCTTTGACTGCGCAAGATATTCAAATATATGATATTAAC 2392
 Db 2507 AATGTGATGAAATATGAGACCTTTGACTGCGCAAGATATTCAAATATATGATATTAAC 2566
 Qy 2393 AAAAAGACCAATGAGGCGGCTTCAATCAAGTATGAGTCTCAGAAAGCCCTGTTGAT 2452
 Db 2567 AAAAAGACCAATGAGGCGGCTTCAATCAAGTATGAGTCTCAGAAAGCCCTGTTGAT 2626
 Qy 2453 AGAGTATACATCATCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2512
 Db 2627 AGAGTATACATCATCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2686
 Qy 2513 ACTTTAGGGGCTGCGCTTACCCAGGATTCCTGAGAGAACTTTTAAAGCTGCTGAAG 2572
 Db 2687 ACTTTAGGGGCTGCGCTTACCCAGGATTCCTGAGAGAACTTTTAAAGCTGCTGAAG 2746
 Qy 2573 GAAGGACACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2632
 Db 2747 GAAGGACACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2806
 Qy 2633 GACTGTTGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2692
 Db 2807 GACTGTTGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2866
 Qy 2693 GATGGAATTTCTCATCTTCAACAACCAATGAGGAATATCTTGACCTCAGCCAACTCTCGAA 2752
 Db 2867 GATGGAATTTCTCATCTTCAACAACCAATGAGGAATATCTTGACCTCAGCCAACTCTCGAA 2926
 Qy 2753 CAGATATCACTAGTATCCCTGACACAAAGAGTCTTGTCTTCAAGAGATGATTTCTGTT 2812
 Db 2927 CAGATATCACTAGTATCCCTGACACAAAGAGTCTTGTCTTCAAGAGATGATTTCTGTT 2986

Qy 2813 TTTTCTCCAGACCCCATGCTTACGAAACATGCTTCCCTCAGTATCCACACATAAAGGC 2872
 Db 2987 TTTTCTCCAGACCCCATGCTTACGAAACATGCTTCCCTCAGTATCCACACATAAAGGC 3046
 Qy 2873 AGTGTAAACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2932
 Db 3047 AGTGTAAACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3106
 Qy 2933 AGCTACACTGACGAGGAGACCATGCTTCCAGAGCTTGTCTTCCACTTTATATATG 2992
 Db 3107 AGCTACACTGACGAGGAGACCATGCTTCCAGAGCTTGTCTTCCACTTTATATATG 3166
 Qy 2993 GATCAGAGAGTAAATTAATTGAAAAGTATGATGATGATGATGATGATGATGATGATG 3052
 Db 3167 GATCAGAGAGTAAATTAATTGAAAAGTATGATGATGATGATGATGATGATGATGATG 3226
 Qy 3053 AAAACTTGTATCTTCCAGAGAGGAGAAAGTCTTGTGAGCAGTGTGACTGC 3106
 Db 3227 AAAACTTGTATCTTCCAGAGAGGAGAAAGTCTTGTGAGCAGTGTGACTGC 3280

RESULT 8
 AEF06407
 ID AEF06407 standard; cDNA; 4574 BP.
 AC AEF06407;
 AC AEF06407;
 DT 23-FEB-2006 (first entry)
 XX
 DE Human fibroblast growth factor receptor 2 cDNA SEQ ID NO 25.
 XX
 KW immunostimulant; cytostatic; antiallergic; antiinflammatory;
 KW antihistobial; cardiovascular-gen.; selectable marker; diagnostic;
 KW prognosis; screening; therapeutic; mastocytosis; leukemia; tumor;
 KW hematological disease; cardiovascular disease; infection; inflammation;
 KW immune disorder; allergy; cancer; neoplasm;
 KW fibroblast growth factor receptor 2; gene; ss.
 XX
 OS Homo sapiens.
 XX
 FX
 FX Key Location/Qualifiers
 FT CDS 593..3061
 FT /tag= a
 FT /product= "Human fibroblast growth factor receptor 2"
 XX
 PN MO2005085851-A2.
 XX
 PD 15-SEP-2005.
 XX
 PF 03-MAR-2005; 2005MO-US007519.
 XX
 PR 03-MAR-2004; 2004US-0549865P.
 XX
 PA (ADRA/) ADRA C N.
 XX
 PI Adra CN;
 XX
 XX WPI; 2006-117706/12.
 DR P-PSDB; AEF06408.
 DR GENBANK; NM_022969.
 XX
 PT Assay for identifying compound that alters physiological property of
 PT granulocyte, by contacting granulocyte with candidate compound that
 PT interacts with granulocyte marker, determining and comparing
 PT physiological property to reference.
 XX
 PS Disclosure; SEQ ID NO 25; 149bp; English.
 XX
 CC The invention describes an assay (M1) for identifying compound that
 CC alters physiological property of a granulocyte, by contacting a
 CC granulocyte with a candidate compound that interacts with a granulocyte-
 CC selective marker, determining physiological property of a granulocyte

CC after contacting with a candidate compound, and comparing the
 CC physiological property to a reference property to determine whether the
 CC candidate compound alters the physiological property of a granulocyte.
 CC (M1) is useful for identifying a compound that alters one or more
 CC physiological property of a granulocyte. (M2) is useful for diagnosing a
 CC granulocyte disorder, or non-neutrophil granulocyte disorder or mast cell
 CC disorder, in a biological sample, where the biological sample is a blood
 CC sample and tissue sample. The non-neutrophil granulocyte disorder is a
 CC basophil or eosinophil disorder, where the basophil disorder is a
 CC basophil-associated tumor or cancer, and the eosinophil-associated tumor
 CC or cancer. The mast cell disorder is a mast cell-associated disease or
 CC cancer. (M5) is useful for treating a granulocyte-associated disease or
 CC mast cell-associated disease. The compound identified by (M1) is useful
 CC for treating a granulocyte or mast cell-associated disease, useful for
 CC diagnosing and treating mast cell disorders such as systemic
 CC mastocytosis, indolent mastocytosis, mast cell leukemia, cutaneous
 CC mastocytosis such as urticaria pigmentosa and telangiectasia macularis
 CC eruptive perstans. (M1) or (C1) is useful for drug discovery, disease
 CC diagnosis and/or prognosis, granulocyte type detection and/or selection
 CC and/or manipulation, and/or therapeutic application. (M1) is useful for
 CC screening compounds to identify those that interact with one or more
 CC cell type selective markers. (M1) is useful in identifying leukocytes and
 CC leukocyte-selective markers, and for diagnostic or prognostic purposes
 CC e.g. allergies, cancers, infectious, basophil disorders such as asthma,
 CC eosinophilic pneumonia, helminthic infestations and eosinophilic
 CC gastrointestinal disorders that includes eosinophilic esophagitis,
 CC eosinophilic gastritis, eosinophilic duodenitis, eosinophilic colitis,
 CC eosinophilic gastroenteritis, and eosinophilic ileitis. (C1) is useful
 CC for treating diseases such as cancer, allergy, inflammation, infections
 CC diseases, cardiovascular disease, other diseases associated with one or
 CC more leukocyte cell types. This sequence encodes human fibroblast growth
 CC factor receptor 2, a granulocyte and/or mast cell-selective marker.

SQ Sequence 4574 BP; 1231 A; 1085 C; 1149 G; 1109 T; 0 U; 0 Other;

Query Match 97.0%; Score 3013.2; DB 15; Length 4574;

Best Local Similarity 99.5%; Pred. No. 0; Mismatches 8; Indels 9; Gaps 7;

Matches 3097; Conservative 0; Mismatches 8; Indels 9; Gaps 7;

QY 1 CCCGCGAAGGTTGGTGGAGCAAG-C-CAAGCTGAGTCTTTCTCTCTCGTTC 59
 Db 168 CTGCGAGCAAGTTGGTGGAGCAAGCAAGCTGAGTCTTTCTCTCTCGTTC 227
 QY 60 CCAATTCGAGGAGCGCGCGGCGTCTGAGTCTTTCTCTCTCTCGTTC 116
 Db 228 CCAATTCGAGGAGCGCGCGGCGTCTGAGTCTTTCTCTCTCTCGTTC 286
 QY 117 G-TGAAGCGGAGGCTTGGCGCGCGGAGCAAGCAAGTCTTTCTCTCTG 175
 Db 287 GCTGAAGCGGAGGCTTGGCGCGCGGAGCAAGCAAGTCTTTCTCTCTG 346
 QY 176 GTTCTCTCGCGCAAGCGCGGCGTCTTCTCTCTCTCTCTCTCTCTCTCT 234
 Db 347 GTTCTCTCGCGCAAGCGCGGCGTCTTCTCTCTCTCTCTCTCTCTCTCT 406
 QY 235 GACAAACAGGTCGCGAGGAGCGTTCATTCAGTGAAGTCTCTCTCTCTCT 293
 Db 407 GACAAACAGGTCGCGAGGAGCGTTCATTCAGTGAAGTCTCTCTCTCTCT 466
 QY 294 CTGCGTCTCTGAGCGCGCGGAGCGTTCATTCAGTGAAGTCTCTCTCTCT 352
 Db 467 CTGCGTCTCTGAGCGCGCGGAGCGTTCATTCAGTGAAGTCTCTCTCTCT 526
 QY 353 AGTGTGAGATGAGATTAAGTCAATGAGATATGAGAGAGACCGGAGATTTG 412
 Db 527 AGTGTGAGATGAGATTAAGTCAATGAGATATGAGAGAGACCGGAGATTTG 586
 QY 413 GTAACATGATGAGTGGGCTGTTTCTCTCTCTCTCTCTCTCTCTCTCTCT 472
 Db 587 GTAACATGATGAGTGGGCTGTTTCTCTCTCTCTCTCTCTCTCTCTCTCT 646
 QY 473 TCCCTGCGCGCGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 532

Db 647 TCCCTGCGCGCGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 706
 QY 533 CCAACCAATTAACCAATCTCTCAACAGAGTGTAGTGGCTGCGCAGGAGTGTG 592
 Db 707 CCAACCAATTAACCAATCTCTCAACAGAGTGTAGTGGCTGCGCAGGAGTGTG 766
 QY 593 GAGTGTGCTGCTGTTGGAAGTGTGCGCGTGTATGATTTGAGATGAGGCTG 652
 Db 767 GAGTGTGCTGCTGTTGGAAGTGTGCGCGTGTATGATTTGAGATGAGGCTG 826
 QY 653 TTGGGGCCCAATATGAGCAGTGTCTTATTTGGGAGTACTTGGATTAAGGCG 712
 Db 827 TTGGGGCCCAATATGAGCAGTGTCTTATTTGGGAGTACTTGGATTAAGGCG 886
 QY 713 CTTAGAGATCTCGGCTCTATGCTTGTACTGCGCAGTATGAGTATGAGTAT 772
 Db 887 CTTAGAGATCTCGGCTCTATGCTTGTACTGCGCAGTATGAGTATGAGTAT 946
 QY 773 TACTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 832
 Db 947 TACTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1006
 QY 833 GTGCGGAGATTTTGTGAGTGAACAGTATCAACAGAGACCAATCTGAGCC 892
 Db 1007 GTGCGGAGATTTTGTGAGTGAACAGTATCAACAGAGACCAATCTGAGCC 1066
 QY 893 ACGAAGAAATGGAAGAGCGCTCTCAATGCTGTGCGCGCGCAACCTGTCAAG 952
 Db 1067 ACGAAGAAATGGAAGAGCGCTCTCAATGCTGTGCGCGCGCAACCTGTCAAG 1126
 QY 953 TGCCAGCGCGGAGGAGAACCAATGCAACCATCGGTGCTGTAAGAAACGGAAG 1012
 Db 1127 TGCCAGCGCGGAGGAGAACCAATGCAACCATCGGTGCTGTAAGAAACGGAAG 1186
 QY 1013 AAGCAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATG 1072
 Db 1187 AAGCAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATG 1246
 QY 1073 GAAAGTGTGCTCCATCTGCAAGAGGAAATTAACCTGTGTAGTGAAGTGA 1132
 Db 1247 GAAAGTGTGCTCCATCTGCAAGAGGAAATTAACCTGTGTGTAGTGAAGTGA 1306
 QY 1133 TCCATCAATCAACAGTATGATGATGATGATGATGATGATGATGATGATGAT 1192
 Db 1307 TCCATCAATCAACAGTATGATGATGATGATGATGATGATGATGATGATGAT 1366
 QY 1193 CAAGCGGAGTGTGCGGCAATGCTTCAAGTGTGTGAGAGAGAGCTGATG 1252
 Db 1367 CAAGCGGAGTGTGCGGCAATGCTTCAAGTGTGTGAGAGAGAGCTGATG 1426
 QY 1253 AAGGTTTACATGATGATGATGATGATGATGATGATGATGATGATGATG 1312
 Db 1427 AAGGTTTACATGATGATGATGATGATGATGATGATGATGATGATGATG 1486
 QY 1313 AGTAATATGAGGCGCGGAGGCTGCTCACTCAAGGTTCTCAAGCACTGCGG 1372
 Db 1487 AGTAATATGAGGCGCGGAGGCTGCTCACTCAAGGTTCTCAAGCACTGCGG 1546
 QY 1373 AGTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1432
 Db 1547 AGTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1606
 QY 1433 ATATGTAAAGTCTTCAATTAATAGGAGAGGAGCAAGCTGTGCTCACTG 1492
 Db 1607 ATATGTAAAGTCTTCAATTAATAGGAGAGGAGCAAGCTGTGCTCACTG 1666
 QY 1493 CCAAAACAGAGAGGCTGTAAGAGAGAGAGATTAAGCTTCCCAAGATCACTG 1552
 Db 1667 CCAAAACAGAGAGGCTGTAAGAGAGAGAGATTAAGCTTCCCAAGATCACTG 1726
 QY 1553 ATAGCAATTAATGATGATGATGATGATGATGATGATGATGATGATGATG 1612
 Db 1727 ATAGCAATTAATGATGATGATGATGATGATGATGATGATGATGATGATG 1786

QY 1613 TGCCGATGAGAAACAAGCAAGAAAGCCAGACTTCAGCAGCCGCGCTGTGCAAG 1672
 Db 1787 TGCCGATGAGAAACAAGCAAGAAAGCCAGACTTCAGCAGCCGCGCTGTGCAAG 1846
 QY 1673 CTGACCAAAAGTATCCCTCGCGGAGACAGGTAAAGTTTCGGCTGAGTCCAGCTCTCC 1732
 Db 1847 CTGACCAAAAGTATCCCTCGCGGAGACAGGTAAAGTTTCGGCTGAGTCCAGCTCTCC 1906
 QY 1733 ATGAATCCCAACACCCCGCTGTGAGGATTAACAACAGCTCTCTTCAACGCGAGACACC 1792
 Db 1907 ATGAATCCCAACACCCCGCTGTGAGGATTAACAACAGCTCTCTTCAACGCGAGACACC 1966
 QY 1793 CCCATGCTGCGAGGGGCTCTCGAGTATGAACCTTCAGAGAGCCCAAAATGGAGTTTCCA 2026
 Db 1967 CCCATGCTGCGAGGGGCTCTCGAGTATGAACCTTCAGAGAGCCCAAAATGGAGTTTCCA 2026
 QY 1853 AGAGATTAAGTGAACCTGCGGCAAGCCCTGGGAGAAAGTTGCTTTGGGCAAGTGTCTAG 1912
 Db 2027 AGAGATTAAGTGAACCTGCGGCAAGCCCTGGGAGAAAGTTGCTTTGGGCAAGTGTCTAG 2086
 QY 1913 GCGGAGAGAGTGGGAATTGCAAAAGCAAGCCCAAGAGGCGGTCAACCTGCGCGTGAAG 1972
 Db 2087 GCGGAGAGAGTGGGAATTGCAAAAGCAAGCCCAAGAGGCGGTCAACCTGCGCGTGAAG 2146
 QY 1973 ATGTTGAAGATGATGCGCAGAGAAAGACCTTTCTGATCTGCTGTGATGAGATGAGATG 2032
 Db 2147 ATGTTGAAGATGATGCGCAGAGAAAGACCTTTCTGATCTGCTGTGATGAGATGAGATG 2206
 QY 2033 ATGAAGATGATTTGGGAAACAAGAAATATGATTAATCTTGTGAGGCTGCAACAGGAT 2092
 Db 2207 ATGAAGATGATTTGGGAAACAAGAAATATGATTAATCTTGTGAGGCTGCAACAGGAT 2266
 QY 2093 GGGCTCTCTATGTCATAGTGTGATGCTCTTAAAGCAACCTCCGAGATACCTCCGA 2152
 Db 2267 GGGCTCTCTATGTCATAGTGTGATGCTCTTAAAGCAACCTCCGAGATACCTCCGA 2326
 QY 2153 GCCCGAGAGCCACCCGGGATGAGTACTCTTATGACATTAACCGTGTCTTGAAGAGAG 2212
 Db 2327 GCCCGAGAGCCACCCGGGATGAGTACTCTTATGACATTAACCGTGTCTTGAAGAGAG 2386
 QY 2213 ATGACCTTCAAGACCTTGTGTGATGACCTTACAGTGGCCAGACGAGATGAGTACTTG 2272
 Db 2387 ATGACCTTCAAGACCTTGTGTGATGACCTTACAGTGGCCAGACGAGATGAGTACTTG 2446
 QY 2273 GCTTCCCAAAATGATTCATGAGATTTAGCAAGCCGAATGTTTGTGTAACAGAAAC 2332
 Db 2447 GCTTCCCAAAATGATTCATGAGATTTAGCAAGCCGAATGTTTGTGTAACAGAAAC 2506
 QY 2333 AATGTGATGAATAGCAAGTCTTGGACTGCGCAGAGATTAACAATATAGATTAATAC 2392
 Db 2507 AATGTGATGAATAGCAAGTCTTGGACTGCGCAGAGATTAACAATATAGATTAATAC 2566
 QY 2393 AAAAAAGCCCAATGAGGCGGCTCCAGTCAAGTGAAGTGTCCAGAAAGCCGTGTGAT 2452
 Db 2567 AAAAAAGCCCAATGAGGCGGCTCCAGTCAAGTGAAGTGTCCAGAAAGCCGTGTGAT 2626
 QY 2453 AGAGTATACACTCATCAGAGTGTGTGCTCTTCCGCGGTGTTAATGTGGAGATCTTC 2512
 Db 2627 AGAGTATACACTCATCAGAGTGTGTGCTCTTCCGCGGTGTTAATGTGGAGATCTTC 2686
 QY 2513 ACTTTAGGGGGCTCGCCCTACCAAGGATTCCTCGTGAAGAACTTTTAAAGTCTGTAAG 2572
 Db 2687 ACTTTAGGGGGCTCGCCCTACCAAGGATTCCTCGTGAAGAACTTTTAAAGTCTGTAAG 2746
 QY 2573 GAAGAGACAGAAATGAGTAAAGCCAGCAAGTGCACCAAGAAAGTGCATGATGATGAGG 2632
 Db 2747 GAAGAGACAGAAATGAGTAAAGCCAGCAAGTGCACCAAGAAAGTGCATGATGATGAGG 2806
 QY 2633 GACTGTTGGCATGAGTGCCTCCCAAGAGCAACGTTCAAGAGTGTGTAAGAAAGCTTG 2692
 Db 2807 GACTGTTGGCATGAGTGCCTCCCAAGAGCAACGTTCAAGAGTGTGTAAGAAAGCTTG 2866

QY 2693 GATCGAATTCGACTCTCAACAACCAATGAGAAATACTTGAACCTCAGCCAACTCTCGAA 2752
 Db 2867 GATCGAATTCGACTCTCAACAACCAATGAGAAATACTTGAACCTCAGCCAACTCTCGAA 2926
 QY 2753 CAGTATTCACCTAGTTAACCTTGCACAAGAAAGTTCTTGTCTTCAAGAGATGATTCGTT 2812
 Db 2927 CAGTATTCACCTAGTTAACCTTGCACAAGAAAGTTCTTGTCTTCAAGAGATGATTCGTT 2986
 QY 2813 TTTTCTCCAGACCCCAATGCTTTACAGAACCAATGCTCTCCAGATTCACACATTAACGGC 2872
 Db 2987 TTTTCTCCAGACCCCAATGCTTTACAGAACCAATGCTCTCCAGATTCACACATTAACGGC 3046
 QY 2873 AGTGTAAACAATGATGATGCTGTCTGCTCTCCCAACAGAGACAGCACTGGAACT 2932
 Db 3047 AGTGTAAACAATGATGATGCTGTCTGCTCTCCCAACAGAGACAGCACTGGAACT 3106
 QY 2933 AGCTACACTGAGCAGGAGACCAATGCTTCCAGAGCTTGTGTCTTCACTGTATATATG 2992
 Db 3107 AGCTACACTGAGCAGGAGACCAATGCTTCCAGAGCTTGTGTCTTCACTGTATATATG 3166
 QY 2993 GATCAGAGAGTAAATTAATTGGAAAAATATCAGCATATGCTAAAGATTTATACGTTG 3052
 Db 3167 GATCAGAGAGTAAATTAATTGGAAAAATATCAGCATATGCTAAAGATTTATACGTTG 3226
 QY 3053 AAAAATTGTATCTTCCCAAGAGAGAGAAAGTTTCTGAGACAGTGAAGCTGC 3106
 Db 3227 AAAAATTGTATCTTCCCAAGAGAGAGAAAGTTTCTGAGACAGTGAAGCTGC 3280

RESULT 9
 ADZ13094
 ID ADZ13094 standard; cDNA; 4485 BP.
 AC ADZ13094;
 XX
 DT 16-JUN-2005 (first entry)
 XX
 DE Human cancer-associated cDNA #188.
 XX
 KW Diagnosis; DNA microarray; microarray; biochip; cancer; neoplasm;
 KW cytoskeletal; gene; ss.
 XX
 OS Homo sapiens.
 XX
 EN W02005031001-A2.
 XX
 PD 07-APR-2005.
 XX
 PF 23-SEP-2004; 2004MO-US031617.
 XX
 PR 23-SEP-2003; 2003US-00669920.
 XX
 PA (CHIR) CHIRON CORP.
 XX
 PI Morris DW, Malandro MS;
 XX
 DR WPI, 2005-273395/28.
 DR P-PDB; ADZ13095.
 XX
 PT Nucleic acid array useful for detecting cancer associated nucleic acid,
 CC comprises two or more nucleic acid probes.
 CC
 PS Disclosure; SEQ ID NO 614; 198bp; English.
 CC
 CC The invention relates to a nucleic acid array for detecting a cancer
 CC associated (CA) nucleic acid, comprising two or more nucleic acid probes.
 CC The invention also relates to a peptide array comprising two or more
 CC isolated polypeptides encoded by a CA nucleic acid sequence, a compound
 CC that binds to a polypeptide, an isolated antibody or its fragment which
 CC binds to a polypeptide, which is prepared by immunizing a host animal
 CC with a composition comprising the polypeptide or its antigen binding
 CC fragment and collecting cells from the host expressing antibodies against
 CC the antigen or its antigen binding fragment, a composition comprising the

QY 1850 CCAAGATAGTGAACACTGCGCAAGCCCTGGGAGAAAGTTGCTTTGGGCAAGTGTTC 1909
DB 2438 CCAAGAGATAGTGAACACTGCGCAAGCCCTGGGAGAAAGTTGCTTTGGGCAAGTGTTC 2497
QY 1910 ATGGCGGAGAGCACTGGGAAATTTGCAAAAGCAAGCCCAAGGAGGCGGTGACCCGTCGCGT 1969
DB 2498 ATGGCGGAGAGCACTGGGAAATTTGCAAAAGCAAGCCCAAGGAGGCGGTGACCCGTCGCGT 2557
QY 1970 AAGATGTTGAAAGATGATGCGCAAGAAAGAACCTTTCTGATCTGTGTGATGATGAG 2029
DB 2558 AAGATGTTGAAAGATGATGCGCAAGAAAGAACCTTTCTGATCTGTGTGATGATGAG 2617
QY 2030 ATGATGAAGTGAATTTGGGAAACCAAGAAATATCATTAATTTCTTGGAGCTTGCACACAG 2089
DB 2618 ATGATGAAGTGAATTTGGGAAACCAAGAAATATCATTAATTTCTTGGAGCTTGCACACAG 2677
QY 2090 GATGGGCTCTCATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2149
DB 2678 GATGGGCTCTCATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2737
QY 2150 CGAGCCCGAGAGCCACCCGGGATGAGTACTCTTATGACATTAACCGTGTCTCTGAGAG 2209
DB 2738 CGAGCCCGAGAGCCACCCGGGATGAGTACTCTTATGACATTAACCGTGTCTCTGAGAG 2797
QY 2210 CAGATGACTTTCAAGACTTGTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 2269
DB 2798 CAGATGACTTTCAAGACTTGTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 2857
QY 2270 TTGGCTTCCCAAAATGATTTCAATCGAGATTTAGCAGCCGAAGATGTTTGTGTAACGAA 2329
DB 2858 TTGGCTTCCCAAAATGATTTCAATCGAGATTTAGCAGCCGAAGATGTTTGTGTAACGAA 2917
QY 2330 AACATGTGATGAAATATGAGCAGCTTTGATCTGCGCAGAGATATCAACATATATGATAT 2389
DB 2918 AACATGTGATGAAATATGAGCAGCTTTGATCTGCGCAGAGATATCAACATATATGATAT 2977
QY 2390 TACAAAAGACCAACCAATGGGCGGCTTCCAGTCAAGTGAATGGCTCCAGAAAGCCCTGTTT 2449
DB 2978 TACAAAAGACCAACCAATGGGCGGCTTCCAGTCAAGTGAATGGCTCCAGAAAGCCCTGTTT 3037
QY 2450 GATAGAGTATACACTCATCAGAGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2509
DB 3038 GATAGAGTATACACTCATCAGAGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3097
QY 2510 TTGACTTTAGGGGGCTGCGCCTTACCCAGGAGATTCCTCCGTGAGAGAACTTTTAAAGCTGTC 2569
DB 3098 TTGACTTTAGGGGGCTGCGCCTTACCCAGGAGATTCCTCCGTGAGAGAACTTTTAAAGCTGTC 3157
QY 2570 AAGGAGAGACACAGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2629
DB 3158 AAGGAGAGACACAGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3217
QY 2630 AGGAGCTGTGGGAGTGGAGTGGCTTCCAGAGACCAAGTTCAGAGAGTGTGTAAGAGAC 2689
DB 3218 AGGAGCTGTGGGAGTGGAGTGGCTTCCAGAGACCAAGTTCAGAGAGTGTGTAAGAGAC 3277
QY 2690 TTGATGAAATTTCTCACTCTTCAACCAATGAGAAATATGATGATGATGATGATGATGATGATGAT 2749
DB 3278 TTGATGAAATTTCTCACTCTTCAACCAATGAGAAATATGATGATGATGATGATGATGATGATGAT 3337
QY 2750 GAAAGATTTCACTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2809
DB 3338 GAAAGATTTCACTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3397
QY 2810 GTTTTCTTCCAGAGCCCATGCTTACAGAAACATGCTTCTCTGATATCCACATTAAC 2869
DB 3398 GTTTTCTTCCAGAGCCCATGCTTACAGAAACATGCTTCTCTGATATCCACATTAAC 3457
QY 2870 GGCAGGTGTTAAACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2929
DB 3458 GGCAGGTGTTAAACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3517
QY 2930 CTAAGCTACACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2989

DB 3518 CTAAGCTACACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3577
QY 2990 ATGATGACAGAGGATTAATATTTGAAAAGTATGATGATGATGATGATGATGATGATGATGAT 3048
DB 3578 ATGATGACAGAGGATTAATATTTGAAAAGTATGATGATGATGATGATGATGATGATGATGAT 3636
RESULT 10
ACF91630
ID ACF91630 standard; DNA; 4587 BP.
XX
AC ACF91630;
XX
DT 02-JUN-2005 (first entry)
XX
DE Human SIRS/sepsis diagnostic marker DNA fragment 10490.
XX
KW Systemic inflammatory response syndrome; SIRS; antibacterial;
XX immunosuppressive; antiinflammatory; diagnosis; sepsis; de.
XX
OS Homo sapiens.
XX
PN WC02004087949-A2.
XX
PD 14-OCT-2004.
XX
PF 31-MAR-2004; 2004MO-EP003419.
XX
PR 02-APR-2003; 2003DE-01015031.
XX 08-AUG-2003; 2003DE-01036511.
PR 02-SEP-2003; 2003DE-01040395.
XX
PA (SIRS-) SIRS LAB GMBH.
XX
PI Russwurm S, Reinhardt K, Saluz H, Straube E, Zipfel PF, Deigner H;
XX
DR WPI, 2004-748070/73.
XX
PT In vitro detection of systemic inflammatory response syndrome and related
XX conditions, for e.g. monitoring progression, comprises detecting abnormal
XX expression of disease-related genes.
XX
PS Disclosure, Page; 75pp; German.
XX
CC The invention relates to a novel method for in vitro detection of
XX systemic inflammatory response syndrome (SIRS). The method comprises
XX detecting abnormal expression of disease-related genes, or their
XX associated peptides. The method of the invention demonstrates
XX antibacterial, immunosuppressive and antiinflammatory applications and
XX may be used for early differential diagnosis, monitoring progression,
XX assessing risk, assessing the likely response to treatment and for post
XX mortem diagnosis of systemic inflammatory response syndrome, sepsis and
XX sepsis-like conditions. The recombinant or synthetic nucleic acid
XX sequences of the invention, or derived proteins or peptides, may be
XX useful as calibrants in assays for the specified diseases, for evaluating
XX activity or toxicity in screening for active agents and/or for
XX preparation of agents for treatment or prevention of the specified
XX diseases. The current sequence is that of a human SIRS/sepsis diagnostic
XX marker DNA fragment of the invention. Note: The sequence data for this
XX patent did not form part of the printed specification, but was obtained
XX in electronic format directly from WIPO at ftp.wipo.int/pub/published
XX pct.sequences. Furthermore, a number of arbitrary SRO ID NO.s are
XX disclosed within the specification, however, these have not been taken
XX into account during indexing due to inconsistencies in application and
XX format
SQ Sequence 4587 BP; 1240 A; 1079 C; 1150 G; 1118 T; 0 U; 0 Other;
Query Match 93.5%; Score 2904.2; DB 13; Length 4587;
Best Local Similarity 97.3%; Pred. No. 0;
Matches 3034; Conservative 0; Mismatches 63; Indels 22; Gaps 7;

[illegible]

Db	1248	AAAGTGTGTGTCCTTCTGACAGAGGAAATTATACCTGTGTGTGAGAAATGAATACGGT	1307
Qy	1134	CCATCAATTCACACGTACACCTGTGATGTTGTGAGCGATCGCTCACCGGCCCATCTCC	1193
Db	1308	CCATCAATTCACACGTACACCTGTGATGTTGTGAGCGATCGCTCACCGGCCCATCTCC	1367
Qy	1194	AAGCCGGACTGCGCGCAATATGCTTCCACATGTGTGCGAGAGACGTATGTTGTCTGCA	1253
Db	1368	AAGCCGGACTGCGCGCAATATGCTTCCACATGTGTGCGAGAGACGTATGTTGTCTGCA	1427
Qy	1254	AGTTTACAGTATGAGCCACAGCCCAATCCAGTGTGAATCAACGACGTGTGAAAAGACGGCA	1313
Db	1428	AGTTTACAGTATGAGCCACAGCCCAATCCAGTGTGAATCAACGACGTGTGAAAAGACGGCA	1487
Qy	1314	GTAATATCGGCGCCGACGGGCTGCTCACTCAAGTTCCTCAAGCACTCGGGGATAAATA	1373
Db	1488	GTAATATCGGCGCCGACGGGCTGCTCACTCAAGTTCCTCAAGCACTCGGGGATAAATA	1547
Qy	1374	GTTCCAAATGCAAGATGCTGCTGTG-----TCAATGTGACCGAGCGGATGCTGGG	1427
Db	1548	CCACGGACAAAGAAATTTGAGGTTCTCTAATATTCGGAATGTAACTTTTGAAGACCTGTGGG	1607
Qy	1428	AATATATATGTAAAGTCTCCAAATTATATATGAGCGCAACAGCTCTGCGCTCACTG	1487
Db	1608	AATATATGCTGTTTGGCGGGTAAATTCATATGGAATATCTTTCACTGTGCAATGTGACAG	1667
Qy	1488	TCCGACCAAAACACAAAGCGCGCTGGAAGAGAAAAGAGATTACAGTTTCCACAGCTAAC	1547
Db	1668	TTCTGTCC-----AGCGCTGGAAAGAGAAAAGAGATTACAGCTTCCACAGCTAAC	1718
Qy	1548	TGAGATATGCACTTATCTGCATATAGGGGTCTTTTAATGCGCTGTATGTGTGTAACTGCA	1607
Db	1718	TGAGATATGCACTTATCTGCATATAGGGGTCTTTTAATGCGCTGTATGTGTGTAACTGCA	1778
Qy	1608	TCCGTGCGCGGATGAAGAACACGACCAAAGAGCGACCTTCAGAGCGACGCGGCTGTGC	1667
Db	1778	TCCGTGCGCGGATGAAGAACACGACCAAAGAGCGACCTTCAGAGCGACGCGGCTGTGC	1838
Qy	1668	ACAAGCTGACCAAAAGTATCCCTCTGCGAGACAGGTACAGTTTTCGCTGAGTCAAGT	1727
Db	1838	ACAAGCTGACCAAAAGTATCCCTCTGCGAGACAGGTACAGTTTTCGCTGAGTCAAGT	1898
Qy	1728	CCTCCATGAATCTCAACAACCCCGCTGTGTGAGATTAACAACGCTCTCTTCAACGGCAG	1787
Db	1898	CCTCCATGAATCTCAACAACCCCGCTGTGTGAGATTAACAACGCTCTCTTCAACGGCAG	1958
Qy	1788	ACAACCCCAATCTGTGCAAGGGTCTTCCGATGTAACTTCCAGAGACCCCAAAATGGGAGT	1847
Db	1958	ACAACCCCAATCTGTGCAAGGGTCTTCCGATGTAACTTCCAGAGACCCCAAAATGGGAGT	2018
Qy	1848	TTCCAAGAGATAGCTGACACTGTGGCAAGCCCTGTGGAGAAAGTGTGCTTTTGGCAATGG	1907
Db	2018	TTCCAAGAGATAGCTGACACTGTGGCAAGCCCTGTGGAGAAAGTGTGCTTTTGGCAATGG	2078
Qy	1908	TCATGTGCGGAAGCAGTGTGAATTGACAAAGCAAGCCCAAGAGAGCGGTCAACGTTGCGG	1967
Db	2078	TCATGTGCGGAAGCAGTGTGAATTGACAAAGCAAGCCCAAGAGAGCGGTCAACGTTGCGG	2138
Qy	1968	TGAAGATTTTAAAGATGATGCTCACAGAGAAAGCTTTTCTGATCTGTGTCAAGATGG	2027
Db	2138	TGAAGATTTTAAAGATGATGCTCACAGAGAAAGCTTTTCTGATCTGTGTCAAGATGG	2198
Qy	2028	AGATGATGAAGTATTTGGGAAAACAAGAAATATCATAAATCTTCTTGGAGCTGCAAC	2087
Db	2198	AGATGATGAAGTATTTGGGAAAACAAGAAATATCATAAATCTTCTTGGAGCTGCAAC	2258
Qy	2088	AGATGAGGCTCTCTATATCTAATGTGAATGTGATGTGCTTAAAGCAACCTCCGAGATATCC	2147
Db	2258	AGATGAGGCTCTCTATATCTAATGTGAATGTGATGTGCTTAAAGCAACCTCCGAGATATCC	2318
Qy	2148	TCCGAGCCCGAGGCAACCCGGATGGAATCTCTATGACATTAACGTTGCTGTAGG	2207

Db 2319 TCCGAGCCCGAGGCCACCCGGAGTGAAGTACTCTTATGACATTAACCTGTTCTCGAGG 2378
 Qy 2208 AGCAGATGACCTTTCAAGAGCTTGTGTGTCATGCACTACCAAGCTGGCCAGACGGATGAGT 2267
 Db 2379 AGCAGATGACCTTTCAAGAGCTTGTGTGTCATGCACTACCAAGCTGGCCAGACGGATGAGT 2438
 Qy 2268 ACTTGGCTTCCCAAAATGATTTATCATGAGATTTAGCAGCCAGAAATGTTTTGTATACG 2327
 Db 2439 ACTTGGCTTCCCAAAATGATTTATCATGAGATTTAGCAGCCAGAAATGTTTTGTATACG 2498
 Qy 2328 AAAACAAATGATGAAATATGAGACTTGTGAGCTGGCCAGATATCAAAATATAGACT 2387
 Db 2499 AAAACAAATGATGAAATATGAGACTTGTGAGCTGGCCAGATATCAAAATATAGACT 2558
 Qy 2388 ATTACAAAAGACCAACCAATGGGCGCTTCCAGTCAAGTGAATGAGTCCAGAAAGCCCTGT 2447
 Db 2559 ATTACAAAAGACCAACCAATGGGCGCTTCCAGTCAAGTGAATGAGTCCAGAAAGCCCTGT 2618
 Qy 2448 TTGATGAGATTAACCTCATCAGATGATGTGTGCTTCCGGGCTTTAATGTGGAGA 2507
 Db 2619 TTGATGAGATTAACCTCATCAGATGATGTGTGCTTCCGGGCTTTAATGTGGAGA 2678
 Qy 2508 TCTTCACTTTAAGGGGCTGGCCCTTACCCAGGAGATCCCGTGGAGAACTTTTAAGCTGC 2567
 Db 2679 TCTTCACTTTAAGGGGCTGGCCCTTACCCAGGAGATCCCGTGGAGAACTTTTAAGCTGC 2738
 Qy 2568 TGAAGGAGAGACACAGAAATGATTAAGCAAGCCAACTGCAACCAAGATGTATCATGATGA 2627
 Db 2739 TGAAGGAGAGACACAGAAATGATTAAGCAAGCCAACTGCAACCAAGATGTATCATGATGA 2798
 Qy 2628 TGAAGGAGCTGTGGCATGAGTCCCTCCAGAGACCAACGTTTCAAGCAGTGTGAAG 2687
 Db 2799 TGAAGGAGCTGTGGCATGAGTCCCTCCAGAGACCAACGTTTCAAGCAGTGTGAAG 2858
 Qy 2688 ACTTGAATGGAATTTCTCACTCTGCAACCAATGAGGAATCTTGAAGCTTCAAGCCAACTTC 2747
 Db 2859 ACTTGAATGGAATTTCTCACTCTGCAACCAATGAGGAATCTTGAAGCTTCAAGCCAACTTC 2918
 Qy 2748 TCGAAGATTAACCTAGTAACTTCACTGACACAAAGATTTCTTCCAGAGATGATT 2807
 Db 2919 TCGAAGATTAACCTAGTAACTTCACTGACACAAAGATTTCTTCCAGAGATGATT 2978
 Qy 2808 CTGTGTTTTCTCGAAGCCCATGCTTTAAGCAACCATGCTTCTCTCAATCCACATTA 2867
 Db 2979 CTGTGTTTTCTCGAAGCCCATGCTTTAAGCAACCATGCTTCTCTCAATCCACATTA 3038
 Qy 2868 ACCGCACTGTTAAACATGAATGATCTGTCTGCTGCTCCCAAGAGAGACAGACTGGG 2927
 Db 3039 ACCGCACTGTTAAACATGAATGATCTGTCTGCTGCTCCCAAGAGAGAGACTGGG 3098
 Qy 2928 AACCTAGCTACACTGAGCAGAGAGACCATGCTTCCAGAGCTTGTGTCTCACTGTAT 2987
 Db 3099 AACCTAGCTACACTGAGCAGAGAGACCATGCTTCCAGAGCTTGTGTCTCACTGTAT 3158
 Qy 2988 ATATGATCAGAGAGATTAATTAATTTGAAAAATGATATGATATGTTAAAGTTATAC 3047
 Db 3159 ATATGATCAGAGAGATTAATTAATTTGAAAAATGATATGATATGTTAAAGTTATAC 3218
 Qy 3048 AGTTGAAAACTTGTATCTTCCAGAGAGAGAAAGTTTCTGAGCAGTGGAGCTGC 3106
 Db 3219 AGTTGAAAACTTGTATCTTCCAGAGAGAGAAAGTTTCTGAGCAGTGGAGCTGC 3277

RESULT 11

AEA81171
 ID AEA81171 standard; DNA; 4587 BP.

AC AEA81171;

DT 25-AUG-2005 (first entry)

DE Human fibroblast growth factor receptor-2 transcript variant 1 DNA.

XX

KM screening; obesity; nutritional disorder; anorectic; ds; gene;
 KM fibroblast growth factor receptor-2; FGF receptor-2; transcript variant.
 OS Homo sapiens.
 PN US2005136465-A1.
 XX 23-JUN-2005.
 PD 22-DEC-2004; 2004US-00019829.
 PF 22-DEC-2003; 2003EP-00104902.
 XX 22-DEC-2003; 2003EP-00104902.
 PA (CLER/) CLERC R. G.
 PA (DUCH/) DUCHATEAU-NGUYEN G.
 PA (GARD/) GARDES C.
 PA (MIZR/) MIZRAHI J.
 PA (OSTE/) OSTENSON C.
 XX Clerc RG, Duchateau-Nguyen G, Gardes C, Mizrahi J, Ostenson C;
 PI WPI; 2005-457507/46.
 DR P-PSDB; AEA81232.
 XX Screening test compounds that reduce and/or prevent obesity involves
 PT contacting cell expressing gene from alpha-two-glycoprotein.
 XX Claim 16; SEQ ID NO 38; 21bp; English.
 XX The invention relates to a novel method for screening for test compounds
 CC that reduce and/or prevent obesity. The method comprises contacting a
 CC cell expressing a gene selected from SEQ ID NO. 1-12 or 25-85, with a
 CC compound. The method of the invention demonstrates anorectic applications
 CC and may be useful for screening for compounds that reduce and/or prevent
 CC obesity. The current sequence is that of the human fibroblast growth
 CC factor receptor-2 transcript variant 1 DNA of the invention. The sequence
 CC listing for the specification can be located via the USPTO web-site.
 XX SQ Sequence 4587 BP; 1240 A; 1079 C; 1150 G; 1118 T; 0 U; 0 Other;
 Query Match 93.5%; Score 2904.2; DB 14; Length 4587;
 Best local Similarity 97.3%; Pred. No. 0;
 Matches 3034; Conservative 0; Mismatches 63; Indels 22; Gaps 7;
 Qy 1 CCCGCGAGCAAAAGTTGGTGGAGGCAAG-CAAGCTGAGTCTTCTTCTCTGTTCC 59
 Db 168 CTCGCGAGCAAAAGTTGGTGGAGGCAAGCCCAAGCTGAGTCTTCTTCTCTGTTCC 227
 Qy 60 CCAAAATCGAGGGGAGCCCGCGGGGCTCATG--GCGCTCTCCGAGCCTGGGTAAGC 116
 Db 228 CCAAAATCGAGGGGAGCCCGCGGGGCTCATGCGCGGCTCTCTCCGAGCCTGGGTAAGC 287
 Qy 117 GTGAAGCCCGGGAGGCTTGGCGCCGCGGAAGACCAAGAGCACTTCTGCGTTGAG 176
 Db 288 GTGAAGCCCGGGAGGCTTGGCGCCGCGGAAGACCAAGAGCACTTCTGCGTTGAG 347
 Qy 177 TTGCTCCCGCAACCCCGGGCTGTGCTTTCTTCATCCCGAACCCAGCGGGGCG-CGGG 235
 Db 348 TTGCTCCCGCAACCCCGGGCTGTGCTTTCTTCATCCCGAACCCAGCGGGGCGCGGG 407
 Qy 236 ACAAGCAGGTGCGGAGGAGGCTTGCATTCAAGTGAATCTGACAGCAGCGGAGCGCG 294
 Db 408 ACAAGCAGGTGCGGAGGAGGCTTGCATTCAAGTGAATCTGACAGCAGCGGAGCGCG 467
 Qy 295 TCGGTTCTGAGCCCAACCGCA-GCTGAAGCATTTGCGGTAGTCATGCTCCGTAGAGAA 353
 Db 468 TCGGTTCTGAGCCCAACCGCAAGCTGAAGCATTTGCGGTAGTCATGCTCCGTAGAGAA 527
 Qy 354 GTGTGCAAGTGGATTAAGTCCACATGAGATATGAAAGAGACCGGGGATTTGTAACG 413
 Db 528 GTGTGCAAGTGGATTAAGTCCACATGAGATATGAAAGAGACCGGGGATTTGTAACG 587
 Qy 414 TAACATGATGACGTGGGCTGTTTCATCTGCTGTGTCATGCAATGAGCAACCTGT 473


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QY 2628 TGAGGAGCTGTTGGCATGAGTGCCTCCCGAGAACAGTTCAAGAGTTGTGANG 2687
    |||
DB 2799 TGAGGGACTGTTGGCATGAGTGCCTCCCGAGAACAGTTCAAGAGTTGTGANG 2858
    |||
QY 2688 ACTTGGATGGAATTTCTCACTCTTCACAAACCAATGAGAAATCTTGACCTCAGCAACCTC 2747
    |||
DB 2859 ACTTGGATGGAATTTCTCACTCTTCACAAACCAATGAGAAATCTTGACCTCAGCAACCTC 2918
    |||
QY 2748 TCGAAGATGATTCACCTAGTTACCTTCAGACACAAGATTCTTGTCTTGAGAGATGAT 2807
    |||
DB 2919 TCGAAGATGATTCACCTAGTTACCTTCAGACACAAGATTCTTGTCTTGAGAGATGAT 2978
    |||
QY 2808 CTGTTTTTCTCCAGACCCCGATCTTACGACACATGCTCTTCTCAATTCACACATTA 2867
    |||
DB 2979 CTGTTTTTCTCCAGACCCCGATCTTACGACACATGCTCTTCTCAATTCACACATTA 3038
    |||
QY 2868 ACGGAGGTGTTAAACATGATGACCTGTCTGCTCCCAAGACAGACAGCACTGGG 2927
    |||
DB 3039 ACGGAGGTGTTAAACATGATGACCTGTCTGCTCCCAAGACAGACAGCACTGGG 3098
    |||
QY 2928 AACCTAGCTACACTGAGAGGAGACATGCTCCCGAGAGCTTGTCTCCACTGTAT 2987
    |||
DB 3099 AACCTAGCTACACTGAGAGGAGACATGCTCCCGAGAGCTTGTCTCCACTGTAT 3158
    |||
QY 2988 ATATGATCAGAGAGATTAATTAATTGAAAAATATCAGATATGTGTAAGATTATAC 3047
    |||
DB 3159 ATATGATCAGAGAGATTAATTAATTGAAAAATATCAGATATGTGTAAGATTATAC 3218
    |||
QY 3048 AGTTGAAAACTTGTATCTTCCCGAGAGAGAAAGTTTGTGAGACAGTGCAGCTGC 3106
    |||
DB 3219 AGTTGAAAACTTGTATCTTCCCGAGAGAGAAAGTTTGTGAGACAGTGCAGCTGC 3277
    |||

RESULT 12
ABE49323
ID ABE49323 standard, cDNA; 4587 BP.
AC ABE49323;
DT 09-FEB-2006 (first entry)
XX Human FGR-2 polynucleotide SEQ ID NO 242.
DB
XX
XX immunosuppressive; cytostatic; nootropic; neuroprotective; antiarthritic;
XX antiinflammatory; antirheumatic; antiviral; pharmaceutical; therapeutic;
XX cell signaling; cell proliferation; angiogenesis; neovascularization;
XX neurodegenerative disease; neuroprotective; neurological disease;
XX inflammation; hyperproliferation; cancer; parasitic infection;
XX antiparasitic; viral infection; viticude; infection;
XX angiogenesis disorder; antiangiogenic; cardiovascular disease; tumor;
XX neoplasm; immune disorder; cell surface receptor; ds.
XX
OS Homo sapiens.
XX
XX WO2005113596-A2.
XX
XX 01-DEC-2005.
XX
XX 13-MAY-2005; 2005MO-US017051.
XX
XX 14-MAY-2004; 2004US-0571289P.
XX 18-JUN-2004; 2004US-0580990P.
XX 30-MAR-2005; 2005US-066825P.
XX
XX (RECE-) RECEPTOR BIOLOGIX INC.
XX
XX Jin P, Shepard MH;
XX
XX WPI; 2005-812226/82.
XX
XX P-Psdb; ABE49350.
XX
XX New polypeptides, specifically isoforms of cell surface receptors, such

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PT as EphA, VEGF, MET, RON, CSF, etc, useful treating cancer, or
PT inflammatory, infectious, angiogenesis-related conditions, or immune
PT disorders.
XX
XX
XX Example 1; SEQ ID NO 242; 647bp; English.
XX
CC The invention describes an isolated polypeptide, comprising at least one
CC domain of an EphA or EphB receptor, where the polypeptide comprises an
CC ephrin ligand binding domain and the polypeptide lacks one or more amino
CC acids corresponding to the transmembrane domain of the EphA or EphB
CC receptor where the membrane localization of the polypeptide is reduced or
CC abolished compared to the EphA or EphB receptor. The polypeptides,
CC compositions, molecules and methods are useful for treating cancers,
CC inflammatory diseases, infectious diseases angiogenesis-related
CC conditions (conditions involving angiogenesis), cell proliferation-
CC related conditions, conditions involving hyperproliferation of cells,
CC immune disorders and neurodegenerative diseases. The disease or condition
CC is selected from rheumatoid arthritis, multiple sclerosis, posterior
CC intraocular inflammation, uveitic disorders, ocular surface inflammatory
CC disorders, neovascular disease, proliferative vitreoretinopathy,
CC atherosclerosis, rheumatoid arthritis, hemangioma, diabetes mellitus,
CC inflammatory bowel disease, psoriasis, Alzheimer's disease, lupus,
CC vascular stenosis, restenosis, inflammatory joint disease,
CC atherosclerosis, urinary obstructive syndromes, and asthma. The disease
CC or condition is selected from carcinoma, lymphoma, blastoma, sarcoma,
CC leukemia, lymphoid malignancies, squamous cell cancer, small-cell lung
CC cancer, non-small cell lung cancer, adenocarcinoma of the lung, squamous
CC carcinoma of the lung, cancer of the peritoneum, hepatocellular cancer,
CC gastric cancer, stomach cancer, gastrointestinal cancer, pancreatic
CC cancer, glioblastoma, cervical cancer, ovarian cancer, liver cancer,
CC bladder cancer, hepatoma, breast cancer, colon cancer, rectal cancer,
CC colorectal cancer, endometrial or uterine carcinoma, salivary gland
CC carcinoma, kidney/renal cancer, prostate cancer, vulval cancer, thyroid
CC cancer, hepatic carcinoma, anal carcinoma, penile carcinoma, and head and
CC neck cancer. The disease or condition includes infection by a virus or a
CC parasite. The virus is selected from Myxoma virus, Vaccinia virus,
CC Tanpopo virus, Epstein-Barr virus, Herpes simplex virus, Cytomegalovirus,
CC Herpesvirus saimiri, Hepatitis B virus, African swine fever virus,
CC Parvovirus, Human Immune deficiency virus (HIV), Hepatitis C virus,
CC Influenza virus, Respiratory syncytial virus, Measles virus, Vesicular
CC stomatitis virus, Dengue virus and Ebola virus. The combination is useful
CC for treating angiogenic-related disorder, a tumor and/or an immune
CC disorder. This sequence represents a cell surface receptor isoform
CC polynucleotide.
XX
XX Sequence 4587 BP; 1240 A; 1079 C; 1150 G; 1118 T; 0 U; 0 Other;
XX
XX Query Match 93.5%; Score 2904.2; DB 14; Length 4587;
XX Best local similarity 97.3%; Pred. No. 0;
XX Matches 3034; Conservative 0; Mismatches 63; Indels 22; Gaps 7;
XX
QY 1 CCCGCGAGCAAAAGTTGTTGTGAGGCAAG-CAGCGCTAGTCTTCTTCTCTGTTCC 59
    |||
DB 168 CTCGCGAGCAAAAGTTGTTGTGAGGCAAGCGCAAGCTGAGTCTTCTTCTCTGTTCC 227
    |||
QY 60 CCAATCCGAGGCGAGCCCGCGGCGGTGATG---GCGCTCTCCGAGCTGCGGAGTACGC 116
    |||
DB 228 CCAATCCGAGGCGAGCCCGCGGCGGTGATG---GCGCTCTCCGAGCTGCGGAGTACGC 287
    |||
QY 117 GTGAAGCCCGGAGGAGCTTGCGCCGCGGAAGACCAAGAGACCTTTGCGTTTGAG 176
    |||
DB 288 GTGAAGCCCGGAGGAGCTTGCGCCGCGCGAAGACCAAGAGACCTTTGCGTTTGAG 347
    |||
QY 177 TTGCTCCCGCAACCCCGGAGCTTGCTGCTTCTTCATCCGACCAAGCGGAGGC-CGGG 235
    |||
DB 348 TTGCTCCCGCAACCCCGGAGCTTGCTGCTTCTTCATCCGACCAAGCGGAGGC-CGGG 407
    |||
QY 236 ACAACACAGTGGCGGAGAGAGCTTGCCATTGAATGATTCGACAGACAGC-GCAGCGGC 294
    |||
DB 408 ACAACACAGTGGCGGAGAGAGCTTGCCATTGAATGATTCGACAGACAGC-GCAGCGGC 467
    |||
QY 295 TGGGTTCTGAGCCGCAACGCA-GCTGAAGGCAATTGGCGCTAGTCCATGCGGTAGAGAA 353
    |||

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D 468 TCGGTCCTGAGCCACCGCAGGCTGAAGGCAATTGCCGGTAGTCCATGCCGTGAGAGAA 527
Q 354 GTGTGCGAGATGGGATTAACTGCCAATGAGAGATATGGAAGAGACCCGGGATTGGTACG 413
D 528 GTGTGCGAGATGGGATTAACTGCCAATGAGAGATATGGAAGAGACCCGGGATTGGTACG 587
Q 414 TTAACATAGTACGAGGGGGTGTTCATCTGCTGGTCTGGTCTGACCAATGGCACTTGT 473
D 588 TTAACATAGTACGAGGGGGTGTTCATCTGCTGGTCTGGTCTGACCAATGGCACTTGT 647
Q 474 CCCTGGCCCGGCGCTCTTCACTTGAAGATGAGATACCACTTGAAGCCAGAGAGCCAC 533
D 648 CCCTGGCCCGGCGCTCTTCACTTGAAGATGAGATACCACTTGAAGCCAGAGAGCCAC 707
Q 534 CAACCAAAATACCAAAATCTCTCAACCAAGATGTAAGTGGCTGGCCAGGGGAGTGGCTAG 593
D 708 CAACCAAAATACCAAAATCTCTCAACCAAGATGTAAGTGGCTGGCCAGGGGAGTGGCTAG 767
Q 594 AGGTGGCTGGCTGGTGAAGATGCCGCCGTGATCAAGTGGATTAAGGATGGGGTGAAT 653
D 768 AGGTGGCTGGCTGGTGAAGATGCCGCCGTGATCAAGTGGATTAAGGATGGGGTGAAT 827
Q 654 TGGGGCCCAACAAATAGAGCAGTGTATTGGGGAGTACTTGACATTAAGGGCCCAAC 713
D 828 TGGGGCCCAACAAATAGAGCAGTGTATTGGGGAGTACTTGACATTAAGGGCCCAAC 887
Q 714 CTAGAGACTCGGCTCTTATGCTTGTATCTGCCAGTGAAGCTGTGAAGCTTGT 773
D 888 CTAGAGACTCGGCTCTTATGCTTGTATCTGCCAGTGAAGCTGTGAAGCTTGT 947
Q 774 ACTTCATGATGTAATGTCAAGATGCCATCTCATCCGAGATGAGAGATGACCCATG 833
D 948 ACTTCATGATGTAATGTCAAGATGCCATCTCATCCGAGATGAGAGATGACCCATG 1007
Q 834 GTGCGGAAGATTTGTCACTGAGAAACAGTAAACAAGAAGACCACTACTGACCA 893
D 1008 GTGCGGAAGATTTGTCACTGAGAAACAGTAAACAAGAAGACCACTACTGACCA 1067
Q 894 CAGAAAAGATGAAAAGCGGCTCAATGCTGCTCGCGGCAACACTGTCAAGTTTGGCT 953
D 1068 CAGAAAAGATGAAAAGCGGCTCAATGCTGCTCGCGGCAACACTGTCAAGTTTGGCT 1127
Q 954 GCCCAGCGGGGGGAAACCAATGCAACCAATGCGGTGCTGAAAACCGGGAAGAGTTTA 1013
D 1128 GCCCAGCGGGGGGAAACCAATGCAACCAATGCGGTGCTGAAAACCGGGAAGAGTTTA 1187
Q 1014 AGCAGAGCATCGATTTGAGAGGCTACAAGTACGAAAACAGCAGTGGAGCTCATTAATG 1073
D 1188 AGCAGAGCATCGATTTGAGAGGCTACAAGTACGAAAACAGCAGTGGAGCTCATTAATG 1247
Q 1074 AAAGTGTGCTCCATCTGACAAAGGAAATTAATACCTGTGTAGTGAAGATGAATACGGGT 1133
D 1248 AAAGTGTGCTCCATCTGACAAAGGAAATTAATACCTGTGTGTGAGAAATGAATACGGGT 1307
Q 1134 CCATCAATCAAGCTACCTGATGTTGTGAGAGCATGCTCCACCGGCCCATCTCTCC 1193
D 1308 CCATCAATCAAGCTACCTGATGTTGTGAGAGCATGCTCCACCGGCCCATCTCTCC 1367
Q 1194 AAGCCGAGCTGCGGCAAAATGCTCAACAGTGTGCGAGAGAGAGTGAAGTTTGTCTCA 1253
D 1368 AAGCCGAGCTGCGGCAAAATGCTCAACAGTGTGCGAGAGAGAGTGAAGTTTGTCTCA 1427
Q 1254 AGGTTTACAGTATGCCAGGCCCAATCAAGTGGATCAAGCAGTGAAGAAAGACGCA 1313
D 1428 AGGTTTACAGTATGCCAGGCCCAATCAAGTGGATCAAGCAGTGAAGAAAGACGCA 1487
Q 1314 GTAATATAGGGGCGGAGGCTGCTTCAAGTGTCTCAAGCTCGGGAGTAATA 1373
D 1488 GTAATATAGGGGCGGAGGCTGCTTCAAGTGTCTCAAGCTCGGGAGTAATA 1547
Q 1374 GTTCAATGACAGATGCTGCTGT-----TCAATGACAGAGGCGGATGCTGGGG 1427
D 1548 CCAAGGACAAAGATGAGGTTCTTATATTCCGAGATGAATCTTTGAGAGACCTGGGG 1607

Q 1428 AATATATAGTAAGTCTCCAAATTAATAGGGGAGGCCAACAAGTCTGCTGCTCACTG 1487
D 1608 AATATATAGTCTTGGCGGGTAATTTCTATGGGATATCTTTCACTCTGCAATGGTTGACAG 1667
Q 1488 TCCGCGCAAAACAGCAAGCCCTGGAAGAGAAAAAGATTAACAGTTCCCGACATAC 1547
D 1668 TTTCTGCC-----AGGCGCTGGAAGAGAAAAAGAGATTAACAGTTCCCGACATAC 1718
Q 1548 TGAATATAGCATTTTACTGCAATAGGGGTCTTTTAAATGCGCTGTATGGTGTAAACATCA 1607
D 1719 TGAATATAGCATTTTACTGCAATAGGGGTCTTTTAAATGCGCTGTATGGTGTAAACATCA 1778
Q 1608 TCCGTGCGGAATGAAGAACACGACCAAGAGCCAGACTTCAGAGCCAGCGGCTGTC 1667
D 1779 TCCGTGCGGAATGAAGAACACGACCAAGAGCCAGACTTCAGAGCCAGCGGCTGTC 1838
Q 1668 ACAAGCTGACCAAAACGTATCCCTGCGGAGACAGGTAAAGTTTCGGCTGATGTCAGCT 1727
D 1839 ACAAGCTGACCAAAACGTATCCCTGCGGAGACAGGTAAAGTTTCGGCTGATGTCAGCT 1898
Q 1728 CTTCCATGAATCTCAACACCCCGCTGGTGAAGATTAACAACGCTCTTCAACGGCAG 1787
D 1899 CTTCCATGAATCTCAACACCCCGCTGGTGAAGATTAACAACGCTCTTCAACGGCAG 1958
Q 1788 ACAACCCCAATGCTGGAGGGGGTCTCCGAGTATGAATCCAGAGGACCCCAAAATGGAGT 1847
D 1959 ACAACCCCAATGCTGGAGGGGGTCTCCGAGTATGAATCCAGAGGACCCCAAAATGGAGT 2018
Q 1848 TTCCAAGAGATTAAGCTGACACTGGGCAAGCCCTGAGAGAGGTTGCTTTGGCAATGG 1907
D 2019 TTCCAAGAGATTAAGCTGACACTGGGCAAGCCCTGAGAGAGGTTGCTTTGGCAATGG 2078
Q 1908 TCATGCGGAAGCAGTGGAAATGACAAAGACAAAGCCCAAGAGGCGGTACCGTGGCCG 1967
D 2079 TCATGCGGAAGCAGTGGAAATGACAAAGACAAAGCCCAAGAGGCGGTACCGTGGCCG 2138
Q 1968 TGAAGATGTTGAAAAGATGATGCCACAGAGAAAGCTTTTGATCTGGTGCAGAGATGG 2027
D 2139 TGAAGATGTTGAAAAGATGATGCCACAGAGAAAGCTTTTGATCTGGTGCAGAGATGG 2198
Q 2028 AGATGATGAAGATGATTTGGGAAAACAAGAAATATCATAAATCTTCTTGGAGCCTGCACAC 2087
D 2199 AGATGATGAAGATGATTTGGGAAAACAAGAAATATCATAAATCTTCTTGGAGCCTGCACAC 2258
Q 2088 AGATGCGGCTCTCTATGTCAATGTTGATGCTTAAAGGCAACCTCCGAGATACC 2147
D 2259 AGATGCGGCTCTCTATGTCAATGTTGATGCTTAAAGGCAACCTCCGAGATACC 2318
Q 2148 TCCGAGCCCGGAGGCCACCCGGGATGGAATCTCTATGACATTAACCGTGTCTGAGG 2287
D 2319 TCCGAGCCCGGAGGCCACCCGGGATGGAATCTCTATGACATTAACCGTGTCTGAGG 2378
Q 2208 AGCAGATGACCTTCAAGAGCTTGGTGTATGCACTGACCTACAGCTGGCCAGACGATGAGT 2267
D 2379 AGCAGATGACCTTCAAGAGCTTGGTGTATGCACTGACCTACAGCTGGCCAGACGATGAGT 2438
Q 2268 ACTTGGCTTCCAAAATGTAATTCATGAGATTTAGAGCCAGAAATGTTTGGTAAACG 2327
D 2439 ACTTGGCTTCCAAAATGTAATTCATGAGATTTAGAGCCAGAAATGTTTGGTAAACG 2498
Q 2328 AAAAATATGATGAAAATATGACAGCTTTGAGCTGGCAGAGATTAACAATTAAGT 2387
D 2499 AAAAATATGATGAAAATATGACAGCTTTGAGCTGGCAGAGATTAACAATTAAGT 2558
Q 2288 ATTACAAAAGACCAACCAATGGGGGCTTCAAGTGAATGAGTCTCCAGAAAGCCCTGT 2447
D 2559 ATTACAAAAGACCAACCAATGGGGGCTTCAAGTGAATGAGTCTCCAGAAAGCCCTGT 2618
Q 2448 TTGATAGATTAACACTCAATCAAGTATGTTGTCTTTCCGGGCTTTAATGTGGAGA 2507
D 2619 TTGATAGATTAACACTCAATCAAGTATGTTGTCTTTCCGGGCTTTAATGTGGAGA 2678

QY 2508 TCTTCACTTTAGGGGCTCGCCCTACCAAGGATTCGCGTGAAGAACTTTTAACTTC 2567
| | | | |
Db 2679 TCTTCACTTTAGGGGCTCGCCCTACCAAGGATTCGCGTGAAGAACTTTTAACTTC 2738
| | | | |
QY 2568 TGAAGAAAGACACAGAAATGATTAAGCCCAACCTGCACCAACCACTGATCATGATTA 2627
| | | | |
Db 2739 TGAAGAAAGACACAGAAATGATTAAGCCCAACCTGCACCAACCACTGATCATGATTA 2798
| | | | |
QY 2628 TGAAGGACTGTTGGCATGACAGTCCCTCCAGAGCAACAGTTTCAAGCATTTGTAGAAG 2687
| | | | |
Db 2799 TGAAGGACTGTTGGCATGACAGTCCCTCCAGAGCAACAGTTTCAAGCATTTGTAGAAG 2858
| | | | |
QY 2688 ACTTGATGGAATTTCTCACTCTTCAACCAATGAGAAATCTTGAACCTCAGCAACTTC 2747
| | | | |
Db 2859 ACTTGATGGAATTTCTCACTCTTCAACCAATGAGAAATCTTGAACCTCAGCAACTTC 2918
| | | | |
QY 2748 TGAAGAAAGATTCACCTAGTACCCCTGCACCAAGAAAGTTCTGTTGAGAGATTA 2807
| | | | |
Db 2919 TGAAGAAAGATTCACCTAGTACCCCTGCACCAAGAAAGTTCTGTTGAGAGATTA 2978
| | | | |
QY 2808 CTGTTTTTCTCCAGACCCCATGCTTACCAACCATGCTTCTCAGTATCCACATTA 2867
| | | | |
Db 2979 CTGTTTTTCTCCAGACCCCATGCTTACCAACCATGCTTCTCAGTATCCACATTA 3038
| | | | |
QY 2868 ACGGCAGTGTTAAACATGATGATCTGTCTGCTGCTGCCAAACAGACAGCACTGG 2927
| | | | |
Db 3039 ACGGCAGTGTTAAACATGATGATCTGTCTGCTGCTGCCAAACAGACAGCACTGG 3098
| | | | |
QY 2928 AACCTGCTACACCTGAGGAGGAGACCATGCTCCAGAGCTTGTCTCCACTGTAT 2987
| | | | |
Db 3099 AACCTGCTACACCTGAGGAGGAGACCATGCTCCAGAGCTTGTCTCCACTGTAT 3158
| | | | |
QY 2988 ATATGATCAGAGAGATTAATTAATGAAAGTATCAGCATATGTTAAAGTTATAC 3047
| | | | |
Db 3159 ATATGATCAGAGAGATTAATTAATGAAAGTATCAGCATATGTTAAAGTTATAC 3218
| | | | |
QY 3048 AGTTGAAACTTGTATCTTCCCAAGAGAGAAAGTTTCTGAGCAGTGAATGC 3106
| | | | |
Db 3219 AGTTGAAACTTGTATCTTCCCAAGAGAGAAAGTTTCTGAGCAGTGAATGC 3277
| | | | |
RESULT 13
ADZ13056
ID ADZ13056 standard; cDNA; 4609 BP.
XX
AC ADZ13056;
XX
DT 16-JUN-2005 (first entry)
XX
DE Human cancer-associated cDNA #169.
XX
KM Diagnosis; DNA microarray; microarray; biochip; cancer; neoplasm;
XX
KM cytolethic; gene; ss.
OS Homo sapiens.
XX
PN W02005031001-A2.
XX
PD 07-APR-2005.
XX
PF 23-SEP-2004; 2004WO-US031617.
XX
PR 23-SEP-2003; 2003US-00669920.
XX
PA (CHIR) CHIRON CORP.
XX
PI Morris DW, Malandro MS;
XX
DR MPI; 2005-273395/28.
XX
XX P-PSDB; ADZ13057.
PT Nucleic acid array useful for detecting cancer associated nucleic acid,
comprises two or more nucleic acid probes.

XX
PS Disclosure: SEQ ID NO 576; 199bp; English.
XX
XX The invention relates to a nucleic acid array for detecting a cancer
XX associated (CA) nucleic acid, comprising two or more nucleic acid probes.
XX The invention also relates to a peptide array comprising two or more
XX isolated polypeptides encoded by a CA nucleic acid sequence, a compound
XX that binds to a polypeptide, an isolated antibody or its fragment which
XX binds to a polypeptide, which is prepared by immunizing a host animal
XX with a composition comprising the polypeptide or its antigen binding
XX fragment and collecting cells from the host expressing antibodies against
XX the antigen or its antigen binding fragment, a composition comprising the
XX antibody and a carrier, a method of screening for anticancer activity, a
XX method of detecting a CA nucleic acid, a method of diagnosing cancer, a
XX method of treating cancer and a method of inhibiting expression of a CA
XX nucleic acid in a cell. The CA nucleic acids are useful for detecting CA
XX nucleic acids. The antibody is useful for detecting the presence or
XX absence of cancer cells in an individual which involves contacting cells
XX from the individual with the antibody and detecting a complex of a CA
XX protein from the cancer cells and the antibody, where the detection of
XX the complex correlates with the presence of cancer cells in the
XX individual. The composition is useful for inhibiting growth of cancer
XX cells in an individual or for delivering a therapeutic agent to cancer
XX cells in an individual. The invention is also useful for diagnosing
XX cancer, for treating cancer and for inhibiting expression of a CA gene in
XX a cell. This sequence represents human cancer-associated cDNA of the
XX invention.
SQ Sequence 4609 BP; 1231 A; 1085 C; 1165 G; 1128 T; 0 U; 0 Other;
Query Match 93.1%; Score 2890.2; DB 14; Length 4609;
Best Local Similarity 97.2%; Pred. No. 0;
Matches 3034; Conservative 0; Mismatches 63; Indels 26; Gaps 8;
QY 1 CCCGAGCAAAAGTTGTGAGGACG-CAGGCTGATCTTCTCTCTGCTCC 59
| | | | |
Db 187 CTGGAGCAAAAGTTGTGAGGACGCAAGCTGATCTTCTCTCTGCTCC 246
| | | | |
QY 60 CCAATCCGAGGACAGCCCGCGGCTCATG--GCGTCTCCGAGCTTGGGTACCC 116
| | | | |
Db 247 CCAATCCGAGGACAGCCCGCGGCTCATG--GCGTCTCCGAGCTTGGGTACCC 306
| | | | |
QY 117 GTGAAGCCCGGAGAGGTTGGCGCCGCGAAGCCCAAGGACCACTTCTGCTTGGAG 176
| | | | |
Db 307 GTGAAGCCCGGAGAGGTTGGCGCCGCGAAGCCCAAGGACCACTTCTGCTTGGAG 366
| | | | |
QY 177 TTGCTCCCGCAACCCCGGCTGTCGCTTCTCCATCCCAACCGCGGAGC-CGGG 235
| | | | |
Db 367 TTGCTCCCGCAACCCCGGCTGTCGCTTCTCCATCCCAACCGCGGAGC-CGGG 426
| | | | |
QY 236 ACAACACAGGTGCGGAGAGAGGTTGCCATTCAGTATCGACAGCAGC-GCAGGCGC 294
| | | | |
Db 427 ACAACACAGGTGCGGAGAGAGGTTGCCATTCAGTATCGACAGCAGC-GCAGGCGC 486
| | | | |
QY 295 TGGGTTCTGAGCCCAACGCA-GCTGAAGCAATGCGGTAGTCCATGCGCGTAGAGAA 353
| | | | |
Db 487 TGGGTTCTGAGCCCAACGCGAGCTGAAGCAATGCGGTAGTCCATGCGCGTAGAGAA 546
| | | | |
QY 354 GTGTGAGATGAGATTAAGTCCATGAGATATGAAAGAGACCGGGAATTTGTACCG 413
| | | | |
Db 547 GTGTGAGATGAGATTAAGTCCATGAGATATGAAAGAGACCGGGAATTTGTACCG 606
| | | | |
QY 414 TAAACATGTCAGTGGGCTGTTTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 473
| | | | |
Db 607 TAAACATGTCAGTGGGCTGTTTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 666
| | | | |
QY 474 CCCTGACCGGCGCTCTCAGTTAGTGAAGATCCACATTTAGGCGCAAGAGCCAC 533
| | | | |
Db 667 CCCTGACCGGCGCTCTCAGTTAGTGAAGATCCACATTTAGGCGCAAGAGCCAC 726
| | | | |
QY 534 CAACCAATACCAATCTCTCAACAGAGTATCTGCTGCGGCGAGGAGTCTGCTAG 593
| | | | |
Db 727 CAACCAATACCAATCTCTCAACAGAGTATCTGCTGCGGCGAGGAGTCTGCTAG 786
| | | | |

QY 594 AGGTGGCTGCTCTGTTGAAAGATGCGCGCTGTATCAAGTTGGACTTAAGATGGGGTGCAC 653
DB AGGTGGCTGCTCTGTTGAAAGATGCGCGCTGTATCAAGTTGGACTTAAGATGGGGTGCAC 846
QY 654 TGGGGCCCAACATAGAGCAGTGTATTGGGGAGTACTTGACAGATTAAGGGCGCCAC 713
DB TGGGGCCCAACATAGAGCAGTGTATTGGGGAGTACTTGACAGATTAAGGGCGCCAC 906
QY 714 CTAGAGCTCCGGCTCTATGCTTGTATCTGCGAGTAGAGCTGTAGACAGTGAACCTTGGT 773
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QY 774 ACTTCATGTTGAATGTCAAGATGCCATCTCATCCGAGATGTAGAGATGACCCGATG 833
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QY 834 GTGCGGAGATTTTGTCAAGTAGAGACAGTAACAACAGAGACCACTATCTGAGCAACA 893
DB GTGCGGAGATTTTGTCAAGTAGAGACAGTAACAACAGAGACCACTATCTGAGCAACA 1086
QY 894 CAGAAAAGATGAGAAAGCGGCTCCATGCTGTGCTGCGCCAACTGTCAAGTTTGGCT 953
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QY 1087 CAGAAAAGATGAGAAAGCGGCTCCATGCTGTGCTGCGCCAACTGTCAAGTTTGGCT 1146
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QY 1267 AAAGTGTGTCCTCATCTGACAGAGGAATTAATCTGTGTAGTGAAGATGAATACGGGT 1326
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OM nucleic - nucleic search, using sw model

Run on: October 2, 2006, 17:37:58 ; Search time 541 Seconds
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Gapop 10.0 , Gapext 1.0

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Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	2806.2	90.3	3080	US-09-954-556-25	Sequence 25, Appl
2	2781.8	89.6	4268	US-09-954-556-3	Sequence 3, Appl
3	2728.6	87.8	2923	US-09-954-556-20	Sequence 20, Appl
4	2723.4	87.7	2826	US-09-954-556-21	Sequence 21, Appl
5	2722	87.6	2868	US-09-954-556-19	Sequence 19, Appl
6	2722	87.6	2941	US-09-954-556-18	Sequence 18, Appl
7	2714.2	87.4	3416	US-08-451-822A-15	Sequence 15, Appl
8	2714.2	87.4	3416	US-08-323-430-15	Sequence 15, Appl
9	2327.4	74.9	3244	US-09-954-556-24	Sequence 24, Appl
10	2320	74.7	2650	US-09-954-556-28	Sequence 28, Appl
11	2320	74.7	2676	US-08-471-570-7	Sequence 7, Appl
12	2201	70.9	3306	US-09-954-556-10	Sequence 10, Appl
13	2072.2	66.7	3025	US-09-954-556-23	Sequence 23, Appl
14	1946	62.7	1954	US-08-471-570-5	Sequence 5, Appl
15	1890.4	60.9	2079	US-09-949-016-3171	Sequence 3171, Ap
16	1890.4	60.9	2079	US-09-949-016-3172	Sequence 3172, Ap
17	1890.4	60.9	2079	US-09-949-016-3173	Sequence 3173, Ap
18	1890.4	60.9	2079	US-09-949-016-3174	Sequence 3174, Ap
19	1890.4	60.9	2079	US-09-949-016-3175	Sequence 3175, Ap
20	1890.4	60.9	2079	US-09-949-016-3176	Sequence 3176, Ap
21	1890.4	60.9	2079	US-09-949-016-3177	Sequence 3177, Ap
22	1890.4	60.9	2079	US-09-949-016-3178	Sequence 3178, Ap
23	1890.4	60.9	2079	US-09-949-016-3179	Sequence 3179, Ap

24	1890.4	60.9	2079	US-09-949-016-3180	Sequence 3180, Ap
25	1823.2	58.7	2310	US-08-471-570-9	Sequence 9, Appl
26	1449.2	46.7	1603	US-08-471-570-3	Sequence 3, Appl
27	1345	43.3	1475	US-09-954-556-27	Sequence 27, Appl
28	1339.8	43.1	2681	US-08-070-165F-9	Sequence 9, Appl
29	1339.8	43.1	2681	US-08-885-418-9	Sequence 9, Appl
30	1269.4	40.9	2675	US-08-070-165F-5	Sequence 5, Appl
31	1269.4	40.9	2675	US-08-885-418-5	Sequence 5, Appl
32	1090	35.1	2469	US-07-997-133-2	Sequence 2, Appl
33	1090	35.1	2469	US-08-459-296-1	Sequence 1, Appl
34	1090	35.1	2469	US-07-997-133-2	Sequence 2, Appl
35	1088.4	35.0	2662	US-08-451-822A-14	Sequence 14, Appl
36	1088.4	35.0	2662	US-08-323-430-14	Sequence 14, Appl
37	1067	34.4	2733	US-08-371-001-14	Sequence 14, Appl
38	1063.6	34.2	2733	PCT-US96-00331-14	Sequence 14, Appl
39	1063.6	34.2	1079	US-08-471-570-13	Sequence 13, Appl
40	1053.6	33.9	3503	US-07-631-717A-1	Sequence 1, Appl
41	1053.6	33.9	3503	US-08-166-717D-1	Sequence 1, Appl
42	1042	33.5	2360	US-09-023-655-1288	Sequence 1288, Ap
43	982.2	31.6	1541	US-09-954-556-26	Sequence 26, Appl
44	921.8	29.7	3944	US-09-949-016-1876	Sequence 1876, Ap
45	921.8	29.7	3944	US-09-949-016-1877	Sequence 1877, Ap

ALIGNMENTS

RESULT 1
US-09-954-556-25
Sequence 25, Application US/09954556
Patent No. 6900053
GENERAL INFORMATION:
APPLICANT: Brett P. Montia
APPLICANT: Susan M. Freiler
APPLICANT: Scott Cooper
TITLE OF INVENTION: ANTISENSE MODULATION OF FIBROBLAST GROWTH FACTOR RECEPTOR 2 EXPRESSION
FILE REFERENCE: RTS-0250
CURRENT APPLICATION NUMBER: US/09/954,556
CURRENT FILING DATE: 2001-09-14
NUMBER OF SEQ ID NOS: 108
SEQ ID NO 25
LENGTH: 3080
TYPE: DNA
ORGANISM: Homo sapiens
FEATURES:
NAME/KEY: CDS
LOCATION: (612)...(3080)
US-09-954-556-25

Query Match 90.3%; Score 2806.2; DB 3; Length 3080;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 2879; Conservative 0; Mismatches 8; Indels 8; Gaps 6;
1 CCCGAGCAAAAGTTGTGAGGCAACG-CAAGCTGAGTCTTCTCTCTGTTCC 59
186 CTCGACGAAAGTTGTGAGGCAACGCAAGCTGAGTCTTCTCTCTGTTCC 245
60 CCAATTCGAGGAGCGGCGGCGGCTGATG---GCGTCTCTCGAGCTTGCGTTACG 116
246 CCAATTCGAGGAGCGGCGGCGGCGGCTGATGCGGCTCTCTCGAGCTTGCGTTACG 305
117 G-TGAAGCCCGAGGAGCTTGCGGCGGCGGCAAGCCCAAGGACCACTTCTGCTTGA 175
306 GCTGAAGCCCGAGGAGCTTGCGGCGGCGGCAAGCCCAAGGACCACTTCTGCTTGA 365
176 GTTGTCTCCCGCAACCCCGGCTGCTGCTTCTCCATCCGACCGCGGCGC-CGGG 234
366 GTTGTCTCCCGCAACCCCGGCTGCTGCTTCTCCATCCGACCGCGGCGC-CGGG 425
235 GACACACAGGTGCGGAGAGCGTTCCATTCAAGTGAAGTGAAGAGC-GCAGCGC 293
426 GACACACAGGTGCGGAGAGCGTTCCATTCAAGTGAAGTGAAGAGC-GCAGCGC 485

QY	294	CTCGGTTCTGAAGCCCAACCCGA- GCTAAGGCATTGGCGCGTAGTCATGCGCCGTAGAGGA	352
Db	486	CTCGGTTCTGAAGCCCAACCCGAGCGTGAAGGCATTGGCGCGTAGTCATGCGCCGTAGAGGA	545
QY	353	AGTGTGAGATGGGATTTAAAGTTCACATGTGAGATATGGAAGAGGACCGGGGATTTGTATCC	412
Db	546	AGTGTGAGATGGGATTTAAAGTTCACATGTGAGATATGGAAGAGGACCGGGGATTTGTATCC	605
QY	413	GTAAACATGTCAAGCTGGGGTCTGTTCACTGCTGGTCTGTGTACCATATGGCAAGAGCCGA	472
Db	606	GTAAACATGTCAAGCTGGGGTCTGTTCACTGCTGGTCTGTGTACCATATGGCAAGAGCCGA	665
QY	473	TCCCTGGCGCCGGCCCTCTCTTCAAGTTTAAATTAAGATACACATTAAGGCCAAGAGCCGA	532
Db	666	TCCCTGGCGCCGGCCCTCTCTTCAAGTTTAAATTAAGATACACATTAAGGCCAAGAGCCGA	725
QY	533	CCAAACCAATATCCAAATCTCTCAACCAAGAAGTATCGTGGCTGGCCAGGGGAGTCCGCTA	592
Db	726	CCAAACCAATATCCAAATCTCTCTCAACCAAGAAGTATCGTGGCTGGCCAGGGGAGTCCGCTA	785
QY	593	GAGGTGCGCTGCTGTGTGAAGAATGCGCGCGTGATCAAGTTGAATTAAGATGGGGTGCAC	652
Db	786	GAGGTGCGCTGCTGTGTGAAGAATGCGCGCGTGATCAAGTTGAATTAAGATGGGGTGCAC	845
QY	653	TTGGGGCCCAACAATAAGGACAGTGTCTTATTTGGGGAGTACTTTCGATTAAGAGGGCGCACA	712
Db	846	TTGGGGCCCAACAATAAGGACAGTGTCTTATTTGGGGAGTACTTTCGATTAAGAGGGCGCACA	905
QY	713	CCTAGAGACTCGGCGCTCTATGCTGTATCTGCACAGTAGACACTGTAGA.CAGTGAACCTTGG	772
Db	906	CCTAGAGACTCGGCGCTCTCTATGCTGTATCTGCACAGTAGAGACTGTAGA.CAGTGAACCTTGG	965
QY	773	TACTTCATGTGTGAATGTCA.CAGATGCCATCTCATCCGGAGATGATGAGAGTAGACCGAT	832
Db	966	TACTTCATGTGTGAATGTCA.CAGATGCCATCTCATCCGGAGATGATGAGAGTAGACCGAT	1025
QY	833	GGTGGGGAAGATTTTGT.CAGTGAACA.CGTAA.CAA.CAAGAAGCACCTACTGGA.CCAAC	892
Db	1026	GGTGGGGAAGATTTTGT.CAGTGAACA.CGTAA.CAA.CAAGAAGCACCTACTGGA.CCAAC	1085
QY	893	ACAGAAAAGATGGAAGGCGGCTCATGCTGTGGCTGGGG.CCA.CA.CGT.CAA.GTTT.CGC	952
Db	1086	ACAGAAAAGATGGAAGGCGGCTCATGCTGTGGCTGGGG.CCA.CA.CGT.CAA.GTTT.CGC	1145
QY	953	TGCCAGCGCGGGGGAACCAATG.CCA.CAATG.CCGTGGCTGTGA.AAA.CGGG.AGAG.TTT	1012
Db	1146	TGCCAGCGCGGGGGAACCAATG.CCA.CAATG.CCGTGGCTGTGA.AAA.CGGG.AGAG.TTT	1205
QY	1013	AAGCAGAGACATCGCATTTGAGAGCTTAA.CAA.GGTA.CGAA.CAAG.CACTGAG.CCTCAT.TATG	1072
Db	1206	AAGCAGAGACATCGCATTTGAGAGCTTAA.CAA.GGTA.CGAA.CAAG.CACTGAG.CCTCAT.TATG	1265
QY	1073	GAAAGTGGTGTCCCAATCTGA.CAAGGGAAATTAT.CTGTGTATGTGAGAAATGAATTA.CGGG	1132
Db	1266	GAAAGTGGTGTCCCAATCTGA.CAAGGGAAATTAT.CTGTGTATGTGAGAAATGAATTA.CGGG	1325
QY	1133	TCCATCAAT.CACA.CGTAC.CACCTGGAATGTTTGTGAG.CGATCG.CCTCA.CCGGCCCAT.CCTC	1192
Db	1326	TCCATCAAT.CACA.CGTAC.CACCTGGAATGTTTGTGAG.CGATCG.CCTCA.CCGGCCCAT.CCTC	1385
QY	1193	CAAGCCGGA.CTGGCCGCAATG.CCTC.CACATGTGTGTGAG.GAGACGTAGA.TTTGTCTGC	1252
Db	1386	CAAGCCGGA.CTGGCCGCAATG.CCTC.CACATGTGTGTGAG.GAGACGTAGA.TTTGTCTGC	1445
QY	1253	AAGGTTTAAAGTAGTGCCCAAGGCCCA.CATCCAGTGGATTC.AAGCA.CGTG.AAA.AGA.CGGC	1312
Db	1446	AAGGTTTAAAGTAGTGCCCAAGGCCCA.CATCCAGTGGATTC.AAGCA.CGTG.AAA.AGA.CGGC	1505
QY	1313	AGTAAATACGGGCGCCGA.CGGGCTG.CCTTAC.CTCAAG.GTTCTTCAAC.CACTCGGGGATTAAT	1372
Db	1506	AGTAAATACGGGCGCCGA.CGGGCTG.CCTTAC.CTCAAG.GTTCTTCAAC.CACTCGGGGATTAAT	1565
QY	1373	AGTTTCAATGC.AAGAGTGTGGCTCTGTTCAATGTGACCGAGCGGATGCTGGGGATAT	1432

Db	1566	AGTTCCAAATCAGAAAGCTGGCTCTGGTTCAATGTGACCTGAGGGGATGTCGGGGAAATAT	1625
Oy	1433	ATATGTAAAGCTCCCAATTATATATAGGGCAGGCCAACAGCTGCGCTGACCTGCTCTG	1492
Db	1626	ATATGTAAAGCTCTCCAAATTATATATAGGGCAGGCCAACAGCTGCGCTGCTCACTGCTCTG	1685
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Db	1686	CCAAAACAGCAAGCGCTGGAAAGAAAAGAAATTACAGCTTCCCAACCTACCTGAG	1745
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Db	1746	ATTAGCCATTTATCTGCATATAGGGGCTTCTTTAATGCGCTGTATGCGGTGAACAAGTACCTG	1805
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Db	1806	TGCGGAATGGAAGAACAGACCAAGAACCCAGACTTCAGACGCCAGCGCGCTGTGCACAG	1865
Oy	1673	CTGACCAAAAGTATCCCGCTGCGGAGACAGGTAAAGATTTCCGCTGAGTCCAGCTCTCC	1732
Db	1866	CTGACCAAAAGTATCCCGCTGCGGAGACAGGTAAAGATTTCCGCTGAGTCCAGCTCTCC	1925
Oy	1733	ATGAACTTCCAACACCCCGCTGTGTGAAGATTAACAAGCGCTCTTCAAGGGCAGACCC	1792
Db	1926	ATGAACTTCCAACACCCCGCTGTGTGAAGATTAACAAGCGCTCTTCAAGGGCAGACCC	1985
Oy	1793	CCCAATGCTGGCAGGGGCTCCAGATATGAACTTCCAGAGAACCCAAAATGGAGTTTCCA	1852
Db	1986	CCCAATGCTGGCAGGGGCTCCAGATATGAACTTCCAGAGAACCCAAAATGGAGTTTCCA	2045
Oy	1853	AGAGATAAGCTGACACTGCGGCAAGCCCTGCGGAGAGAGTTGCTTTGGGCAAGTGTGCATG	1912
Db	2046	AGAGATAAGCTGACACTGCGGCAAGCCCTGCGGAGAGAGTTGCTTTGGGCAAGTGTGCATG	2105
Oy	1913	GCGGAGACAGTGGGAAATTGACAAAGACAAAGCCCAAGAGAGGGGTACACCGTGGCGGTAAg	1972
Db	2106	GCGGAGACAGTGGGAAATTGACAAAGACAAAGCCCAAGAGAGGGGTACACCGTGGCGGTAAg	2165
Oy	1973	ATGTGGAAGAAGTATGCGACAGAGAAGAAACCTTCTGTATCTGCGTGCAGAGATGGAATG	2032
Db	2166	ATGTGGAAGAAGTATGCGACAGAGAAGAAACCTTCTGTATCTGCGTGCAGAGATGGAATG	2225
Oy	2033	ATGAAGATGATTTGGGAAACACAAAGATATCATTAATCTTCTGGAGCCTGCACACAGAT	2092
Db	2226	ATGAAGATGATTTGGGAAACACAAAGATATCATTAATCTTCTGGAGCCTGCACACAGAT	2285
Oy	2093	GGGCTCTCTATGTTCATATGTGAGTATGCTCTTAAAGCAACCTCCGAGATTAACCTCCGA	2152
Db	2286	GGGCTCTCTATGTTCATATGTGAGTATGCTCTTAAAGCAACCTCCGAGATTAACCTCCGA	2345
Oy	2153	GCCCGAGAGCCACCCGGGATGGAAGTACTCTATGACATTTAACCGTGTCTCGAGAGACAG	2212
Db	2346	GCCCGAGAGCCACCCGGGATGGAAGTACTCTCTATGACATTTAACCGTGTCTCGAGAGACAG	2405
Oy	2213	ATGACCTTCAAGGACTTGTGTCTATGACCTTACAGCTGAGCGCAGACGAGTGAATCTTG	2272
Db	2406	ATGACCTTCAAGGACTTGTGTCTATGACCTTACAGCTGAGCGCAGACGAGTGAATCTTG	2465
Oy	2273	GCTTCCCAAAATGTATTCATCGAGATTTAGACCCAGAAATGTTTTGTGTAAACGAAAC	2332
Db	2466	GCTTCCCAAAATGTATTCATCGAGATTTAGACCCAGAAATGTTTTGTGTAAACGAAAC	2525
Oy	2333	AATGTGATGAATAATGACAGACTTTGGAATCCCGCAGAGATATCAACAATATAGACTATTAC	2392
Db	2526	AATGTGATGAATAATGACAGACTTTGGAATCCCGCAGAGATATCAACAATATAGACTATTAC	2585
Oy	2393	AAAAAGACCAACATGCGCGGCTTCCAGTCAAGTGAATGCTCCAGAAAGCCCTGTTGAT	2452
Db	2586	AAAAAGACCAACATGCGCGGCTTCCAGTCAAGTGAATGCTCCAGAAAGCCCTGTTGAT	2645
Oy	2453	AGAGTATCACTCATCAGAGTGAATGTCTGTGCTTCCGGGGTGTATATGTGGGAATCTTC	2512

Db	2646	AGAGTATACACTATCAGAGTGAAGTCTGGTCCCTCGGGGGTGTAATGTGGGAATCTTC	2705
QY	2513	ACTTTAGGGGGCTCGCCCTACCCAGGGATTCGGGTGAGGAACCTTTTAACTGCTGTAAG	2572
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QY	2753	CAGATATCACTACTATTAACCTCGACACAAAGATGTTGTTCTTTAGAGAGATGATTTGTT	2812
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RESULT 2
US-09-954-556-3
: Sequence 3, Application US/09954556
: Patent No. 6900053
: GENERAL INFORMATION:
: APPLICANT: Brett P. Monia
: APPLICANT: Susan M. Freier
: APPLICANT: Scott Cooper
: TITLE OF INVENTION: ANTISENSE MODULATION OF FIBROBLAST GROWTH FACTOR RECEPTOR 2 EXPRESSION
: FILE REFERENCE: RTS-0250
: CURRENT APPLICATION NUMBER: US/09/954,556
: CURRENT FILING DATE: 2001-09-14
: NUMBER OF SEQ ID NOS: 108
: SEQ ID NO 3
: LENGTH: 4268
: TYPE: DNA
: ORGANISM: Homo sapiens
: PEATTRE:
: NAME/KEY: CDS
: LOCATION: (274)...(2739)
: US-09-954-556-3

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Query Match	89.6%;	Score 2781.8;	DB 3;	Length 4268;
Best Local Similarity	97.3%;	Pred. No. 0;		
Matches 2887; Conservative	0;	Mismatches 62;	Indels 18;	Gaps 5;

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Qy	268	AAGTACTGCAGCAGCAGC - GAGCGCTCGGTTCTGAGCCACCGCA - GCTGAGGCA	325
Db	121	AAGTACTGCAGCAGCAGCGCGCTCGGTTCTGAGCCACCGAGCGTGAAGCA	180
Qy	326	TTGGCGCGATCCAGTCCCGTGAAGGAAGTGTGCATGGGATTAAGTCCACATGAGGA	385
Db	181	TTGGCGCGATCCAGTCCCGTGAAGGAAGTGTGCATGAGATTAAGTCCACATGAGGA	240

QY	386	TATGAAAGAGACCGGGGATTTGGTACCGTAAACCATGGTCAGTGGGATCTTTCACTTCG	445
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QY	446	CTGGTCGTGGTCAACATGGCAACCTTGTCCCTGGCCGGCCCTTCCTTCACTTATTTAG	505
Db	301	CTGGTCGTGGTCAACATGGCAACCTTGTCCCTGGCCGGCCCTTCCTTCACTTATTTAG	360
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QY	806	TTCGGAATATATAGATGAACCGAATGGTCGGAATTTTGTCAATGGAACAGTAAC	865

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661 TCCGAGATGATGAGGATGACACCGATGCTGCCGAAGATTTTGTCACTGAGAACACTAAC 720

866 AACAGAGCACCATCTGACCAACAGAAAAAGATGAAAAGCGCTCCATGCTGTG 925

721 AACAGAGACCACTACTGACCAACAGAAAGATGAAAAAGCGCTCCATGCTGTG 780

926 CCTGCGGCAACTGTCAAGTTTGCCTGCCAGCCGGGGGGAACCCAATGCCAACATG 985

781 CTTGCGGCAACACTGTCAAGTTTCGTCGCCAGCGGGGGAAACCAATGCAACCATG 840

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901 CGAACCAGCACTGGAGCCTCAATTATGGAAGTGTGTGCCATCTGACAAGGGAATTAT 960

1106 ACCTGTGTAGTGAGATGATACGGTCCATCAATCACAGTACCACCTGATGTTGNG 1165

961 ACCTGTTGTGGAGATGAATACGGGTCATCATCATCACAGTACCACTGGATGTGTG 1020

1166 GAGCGATCGCTCACCGGCCATCTTCAAGCCGGACTGCCGGCAATGCTTCCAAGTG 1225

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1201 AAGTTCAGGCCCGCCGGTGTAAACCCACGGACAAAGATTTAGGTTCTCAATAT 1260

1401 -TCAATGACCGAGCGGATGCTGGGGAATATATATGTAAAGTCTCCAATTATTAAGG 1459

1261 CGGAATGTAACCTTTTGAGGACGCTGGGGAATATACGTCGTTGGCGGTAATTCATTTGGG 1320

1460 CAGGCCAACCACTCTGCCTGGCTCACTGTCTCTGCCAAAACAGCAAGCGCCTGGAAAGAA 1519

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Db      1321  ATATCTTTCACTGCTGATGTTGACAGTCTGCC-----ACGCGCTGGAGAGAA 1371
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Db      1372  AAGGAGATTACAGCTTCCCAGACTCTGAGATAGCCATTACTGCAATAGGGGTCTTC 1431
Qy      1580  TTAAATGCTGTATGCTGTGTAACAGTCAATCTGTGCGGAATGAAACACGACCAAG 1639
Db      1432  TTAAATGCTGTATGCTGTGTAACAGTCAATCTGTGCGGAATGAAACACGACCAAG 1491
Qy      1640  CCAAGATTACAGAGCCAGCGGCTGTGCAAGCTGACCAAGCTAAGCTATCCCGCGG 1699
Db      1492  CCAAGATTACAGAGCCAGCGGCTGTGCAAGCTGACCAAGCTAAGCTATCCCGCGG 1551
Qy      1700  CAGGTAAAGTTTGGCTGAGTCCAGCTCTCCATGAACTCCAAACCCCGCTGTAG 1759
Db      1552  CAGGTAAAGTTTGGCTGAGTCCAGCTCTCCATGAACTCCAAACCCCGCTGTAG 1611
Qy      1760  ATAAACAACGCTCTCTTCAACGCAACACCCCAATGCTGCAAGGGGTCTCCAGTAT 1819
Db      1612  ATAAACAACGCTCTCTTCAACGCAACACCCCAATGCTGCAAGGGGTCTCCAGTAT 1671
Qy      1820  GAACTTCCAGAGAACCCAAATGGAGTTTCCAAAGATTAAGCTGCACTGGGCAAGCC 1879
Db      1672  GAACTTCCAGAGAACCCAAATGGAGTTTCCAAAGATTAAGCTGCACTGGGCAAGCC 1731
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Db      1852  GACCTTTCGATCTGCTGTGATGATGATGATGATGATGATGATGATGATGATGAT 1911
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Db      1912  ATCATAAATCTTCTGAGAGCTGCAACAGATGGGCTCTCATGTCTATGATGATGAT 1971
Qy      2120  GCCTCTAAAGCAACCTCCGAGAAATCTCCGAGCCCGAGGCCACCCGAGATGAGTAC 2179
Db      1972  GCCTCTAAAGCAACCTCCGAGAAATCTCCGAGCCCGAGGCCACCCGAGATGAGTAC 2031
Qy      2180  TCCCTATGACATTAACCTGTCTTCCGAGAGCAATGACTTTCAAGGACTTGTGTATG 2239
Db      2032  TCCCTATGACATTAACCTGTCTTCCGAGAGCAATGACTTTCAAGGACTTGTGTATG 2091
Qy      2240  ACCCTACGCTGGCCAGAGAGAGATGATGATGATGATGATGATGATGATGATGAT 2299
Db      2092  ACCCTACGCTGGCCAGAGAGAGATGATGATGATGATGATGATGATGATGATGAT 2151
Qy      2300  TTAGCAGCCAGAAATGTTTGTGTAACAGAAACAAATGATGATGATGATGATGAT 2359
Db      2152  TTAGCAGCCAGAAATGTTTGTGTAACAGAAACAAATGATGATGATGATGATGAT 2211
Qy      2360  CTGCGCCAGATATCAACATATGATATTAAGAAAGCCCAATGGCGGCTTCCA 2419
Db      2212  CTGCGCCAGATATCAACATATGATATTAAGAAAGCCCAATGGCGGCTTCCA 2271
Qy      2420  GTCAAGTGAATGCTCCAGAGCCCTGTGATGATGATGATGATGATGATGATGAT 2479
Db      2272  GTCAAGTGAATGCTCCAGAGCCCTGTGATGATGATGATGATGATGATGATGAT 2331
Qy      2480  TGGTCTTCCGGGTGTTAATGTGGAATCTTCACTTAAAGGGGCTGCGCTTACCA 2539
Db      2332  TGGTCTTCCGGGTGTTAATGTGGAATCTTCACTTAAAGGGGCTGCGCTTACCA 2391
Qy      2540  ATTCCCTGAGAGAACTTTTAACTGCTGAAGAGAGACAAATGATGATGATGATGAT 2599

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Db      2392  ATTCCGAGAGAACTTTTAAAGCTGCTGAAGAGACACAGATGATGATGATGATGAT 2451
Qy      2600  AACTGACCAAGAACTGTACATGATGATGAGGACTGTGGCAAGCACTGCCCTCCAG 2659
Db      2452  AACTGACCAAGAACTGTACATGATGATGAGGACTGTGGCAAGCACTGCCCTCCAG 2511
Qy      2660  AGACCAAGGTTCAACAGATGATGATGATGATGATGATGATGATGATGATGATGAT 2719
Db      2512  AGACCAAGGTTCAACAGATGATGATGATGATGATGATGATGATGATGATGATGAT 2571
Qy      2720  GAGGAATCTTGAAGCTTCAAGCACTTCCAAAGATTAAGCTGATGATGATGATGAT 2779
Db      2572  GAGGAATCTTGAAGCTTCAAGCACTTCCAAAGATTAAGCTGATGATGATGATGAT 2631
Qy      2780  AGAAGTTCTTGTCTTCAAGATGATGATGATGATGATGATGATGATGATGATGAT 2839
Db      2632  AGAAGTTCTTGTCTTCAAGATGATGATGATGATGATGATGATGATGATGATGAT 2691
Qy      2840  CGATGCTTCTCAGATTCACACATTAACGAGCTGTTAAACATGATGATGATGATGAT 2899
Db      2692  CGATGCTTCTCAGATTCACACATTAACGAGCTGTTAAACATGATGATGATGATGAT 2751
Qy      2900  GCTGTCCCAACAGACAGCACTGGAACTTACCTAGCTACCTGAGCAGGAGACATGCC 2959
Db      2752  GCTGTCCCAACAGACAGCACTGGAACTTACCTAGCTACCTGAGCAGGAGACATGCC 2811
Qy      2960  TCCAGAGCTTGTGTCTTCACTTGTATATGATGATGATGATGATGATGATGATGAT 3019
Db      2812  TCCAGAGCTTGTGTCTTCACTTGTATATGATGATGATGATGATGATGATGATGAT 2871
Qy      3020  TATACGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3079
Db      2872  TATACGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2931
Qy      3080  AAGAGGTTCTGAGACAGTGAATGCTG 3106
Db      2932  AAGAGGTTCTGAGACAGTGAATGCTG 2958

RESULT 3
US-09-954-556-20
; Sequence 20, Application US/09954556
; Patent No. 690053
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freiler
; APPLICANT: Scott Cooper
; TITLE OF INVENTION: ANTISENSE MODULATION OF FIBROBLAST GROWTH FACTOR RECEPTOR 2 EXPRE
; FILE REFERENCE: RTS-0250
; CURRENT APPLICATION NUMBER: US/09/954,556
; CURRENT FILING DATE: 2001-09-14
; NUMBER OF SEQ ID NOS: 108
; SEQ ID NO 20
; LENGTH: 2923
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (419)...(2872)
US-09-954-556-20

Query Match      87.8%; Score 2728.6; DB 3; Length 2923;
Best Local Similarity 99.0%; Pred. No. 0;
Matches 2746; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

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QY 121 AGCCGGGAGAGCTTGGGCGGCGGAGAGACCACTCTTGTGCGTTGGAGTTC 180
DB 121 AGCCGGGAGAGCTTGGGCGGCGGAGAGACCACTCTTGTGCGTTGGAGTTC 180
QY 181 TCCCGGAGACCCGGGGCTGCTGCTTCTCCATCCGACCCAGCGGGGCGGAGAAC 240
DB 181 TCCCGGAGACCCGGGGCTGCTGCTTCTCCATCCGACCCAGCGGGGCGGAGAAC 240
QY 241 ACAGGTGCGAGAGAGGCTTGCATTCAAGTGACTGAGAGAGAGCGGACGCTCGT 300
DB 241 ACAGGTGCGAGAGAGGCTTGCATTCAAGTGACTGAGAGAGAGCGGACGCTCGT 300
QY 301 CCGAGGCCACCGGAGCTGAAGGATGGCGTATGCTCAATCCGCTGAGAGAGTGA 360
DB 301 CCGAGGCCACCGGAGCTGAAGGATGGCGTATGCTCAATCCGCTGAGAGAGTGA 360
QY 361 GATGGGATTAACGTCCATGAGATATGAGAGAGAGCGGAGATTGTACCGTACAT 420
DB 361 GATGGGATTAACGTCCATGAGATATGAGAGAGAGCGGAGATTGTACCGTACAT 420
QY 421 GGTCAAGCTGGGGTGTTCATCTGCTGTGTGTCACCAATGGCACTTGTCTGTC 480
DB 421 GGTCAAGCTGGGGTGTTCATCTGCTGTGTGTCACCAATGGCACTTGTCTGTC 480
QY 481 CCGGCGCTCTTCACTGTTAGTGAAGATACCACTTGAAGCAGAGACCAACCA 540
DB 481 CCGGCGCTCTTCACTGTTAGTGAAGATACCACTTGAAGCAGAGACCAACCA 540
QY 541 ATACCAATCTCTCAACAGAGATGTAAGTGGCTGCGCCAGGGAGTCTGTAAGTGC 600
DB 541 ATACCAATCTCTCAACAGAGATGTAAGTGGCTGCGCCAGGGAGTCTGTAAGTGC 600
QY 601 CTGCTGTGTAAGAGATCCCGCGTATCACTGATCACTGAAGTGGTGA 660
DB 601 CTGCTGTGTAAGAGATCCCGCGTATCACTGATCACTGAAGTGGTGA 660
QY 661 CAACATAGAGACATGCTTATTTGGGAGTACTTGCAGATTAAGGGCGCCACCTAAGA 720
DB 661 CAACATAGAGACATGCTTATTTGGGAGTACTTGCAGATTAAGGGCGCCACCTAAGA 720
QY 721 CTGCGGCTCTGATCTGTATCTGACAGTGAAGTGTGAAGTGAAGTGAAGTGA 780
DB 721 CTGCGGCTCTGATCTGTATCTGACAGTGAAGTGTGAAGTGAAGTGAAGTGA 780
QY 781 GGTGAATGTCAAGATGCTATCTATCCGAGATGATGAGATGACCCATGCTGCGA 840
DB 781 GGTGAATGTCAAGATGCTATCTATCCGAGATGATGAGATGACCCATGCTGCGA 840
QY 841 AGATTTGTCACTGAGAGACATTAACAGAGAGACCATCTGAGACCAACAGAAA 900
DB 841 AGATTTGTCACTGAGAGACATTAACAGAGAGACCATCTGAGACCAACAGAAA 900
QY 901 GATGAGAAAGGCGCTCATGCTGCTGCGGCAACCTGCAAGTTGCTGCCAGC 960
DB 901 GATGAGAAAGGCGCTCATGCTGCTGCGGCAACCTGCAAGTTGCTGCCAGC 960
QY 961 CCGGGGAGACCCAAATGCGCAACATGCGGTGGCTGAAAAACGGAGAGATTAAAGCA 1020
DB 961 CCGGGGAGACCCAAATGCGCAACATGCGGTGGCTGAAAAACGGAGAGATTAAAGCA 1020
QY 1021 GCATGCACTTGGAGGCTTCAAGGTAACAGAACCACTGAGGCTCATTAATGAGAAAGT 1080
DB 1021 GCATGCACTTGGAGGCTTCAAGGTAACAGAACCACTGAGGCTCATTAATGAGAAAGT 1080
QY 1081 GGTCCCATCTGCAAGGGAATTTATCTGTGTATGAGAGATGAAATCGGCTCATCA 1140
DB 1081 GGTCCCATCTGCAAGGGAATTTATCTGTGTATGAGAGATGAAATCGGCTCATCA 1140
QY 1141 TCACACGTACCACTGAGATGTTGTGAGCAGATGCGCTCAACCGGCTCTCAAGCGG 1200
DB 1141 TCACACGTACCACTGAGATGTTGTGAGCAGATGCGCTCAACCGGCTCTCAAGCGG 1200
QY 1201 ACTGCGGCAAAATGCTTCAACAGTGTGCGAGAGAGAGTGAAGTTGTCTGCAAGTTTA 1260

DB 1201 ACTGCGGCAAAATGCTTCAACAGTGTGCGAGAGAGATGAAGTTGTCTGCAAGTTTA 1260
QY 1261 CAGTATGCTCCAGCCCACTCACTGATGATCAAGACATGAGAGAGAGAGAGAGAGAT 1320
DB 1261 CAGTATGCTCCAGCCCACTCACTGATGATCAAGACATGAGAGAGAGAGAGAGAT 1320
QY 1321 CCGGGCGAGCGGCTGCTCAAGTGTCAAGCACTCGGGGATTAATGTTCCAA 1380
DB 1321 CCGGGCGAGCGGCTGCTCAAGTGTCAAGCACTCGGGGATTAATGTTCCAA 1380
QY 1381 TGCAGAGTGTGCTGCTTCTGATGATGACCGAGCGGATGCTGGGAGATATATATGA 1440
DB 1381 TGCAGAGTGTGCTGCTTCTGATGATGACCGAGCGGATGCTGGGAGATATATATGA 1440
QY 1441 GGTCTCAATTAATATAGGAGAGGCAACAGTCTGCTGCTCACTGCTCCAAACA 1500
DB 1441 GGTCTCAATTAATATAGGAGAGGCAACAGTCTGCTGCTCACTGCTCCAAACA 1500
QY 1501 GCAAGCGCTGAGAGAGAGAGAGATTAAGCTTCCAGACTTACCTGAGATAGCAT 1560
DB 1501 GCAAGCGCTGAGAGAGAGAGAGATTAAGCTTCCAGACTTACCTGAGATAGCAT 1560
QY 1561 TTAATGATAGGGGCTTCTTAATGCTGATATGATGATCACTGCTGCGAAT 1620
DB 1561 TTAATGATAGGGGCTTCTTAATGCTGATATGATGATCACTGCTGCGAAT 1620
QY 1621 GAAGAACAGACAGAGAGGCACTTCAAGAGCAGCGGCTGTGCAAGCTGACCA 1680
DB 1621 GAAGAACAGACAGAGAGGCACTTCAAGAGCAGCGGCTGTGCAAGCTGACCA 1680
QY 1681 AGCTATCCCTGCGAGAGAGAGATTAAGTGGCTGATGATGATGATGATGATGATG 1740
DB 1681 AGCTATCCCTGCGAGAGAGAGATTAAGTGGCTGATGATGATGATGATGATGATG 1740
QY 1741 CAACACCCGCTGAGATTAACAACAGCTCTCTTCAACAGCAGACACCCCATGCT 1800
DB 1741 CAACACCCGCTGAGATTAACAACAGCTCTCTTCAACAGCAGACACCCCATGCT 1800
QY 1801 GCGAGGGGCTCGAGATTAACAACAGCTCTCTTCAACAGCAGACACCCCATGCT 1860
DB 1801 GCGAGGGGCTCGAGATTAACAACAGCTCTCTTCAACAGCAGACACCCCATGCT 1860
QY 1861 GCTGACATGCGGCAAGCCCTGAGAGAGAGTGTGTTGGGCAAGTGTGATGCGAGC 1920
DB 1861 GCTGACATGCGGCAAGCCCTGAGAGAGAGTGTGTTGGGCAAGTGTGATGCGAGC 1920
QY 1921 AGTGGAAATGACAAAGACCAAGGCGGCTGACCGTGGCCGTGAAGTGTGA 1980
DB 1921 AGTGGAAATGACAAAGACCAAGGCGGCTGACCGTGGCCGTGAAGTGTGA 1980
QY 1981 AGATGATGCAAGAGAGAGACCTTCTGATCTGTGTCAAGATGAGATGATGAAT 2040
DB 1981 AGATGATGCAAGAGAGAGACCTTCTGATCTGTGTCAAGATGAGATGATGAAT 2040
QY 2041 GATTGGAAACAGAGATTAATCAATCTTCTGAGGCTGCAACAGATGAGGCTCT 2100
DB 2041 GATTGGAAACAGAGATTAATCAATCTTCTGAGGCTGCAACAGATGAGGCTCT 2100
QY 2101 CTATGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2160
DB 2101 CTATGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2160
QY 2161 GCGACCGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2220
DB 2161 GCGACCGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2220
QY 2221 CAAGGATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2280
DB 2221 CAAGGATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2280
QY 2281 AAATGATTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2340

Db	2281	AAAATGATTCATGCAGATTTTACGACGCCAGAAATGTTTTGGTAAACAGAAAAACATGTGAT	2340
QY	2341	GAATAATGCAGACTTTGGACTCGCCAGAGATATCAACAATATAGACTTATCAAAAAAC	2400
Db	2341	GAATAATGCAGACTTTGGACTCGCCAGAGATATCAACAATATAGACTTATCAAAAAAC	2400
QY	2401	CACCAATGGGGGCTTCAGTCAAGTGGATGGCTCACAAGCCCGTTGGATAGATATA	2460
Db	2401	CACCAATGGGGGCTTCAGTCAAGTGGATGGCTCACAAGCCCGTTGGATAGATATA	2460
QY	2461	CACCTCATCAGATGATGTCGTGCTCTGGGGTGTTAATGTGGAGATCTTCACTTTAGG	2520
Db	2461	CACCTCATCAGATGATGTCGTGCTCTGGGGTGTTAATGTGGAGATCTTCACTTTAGG	2520
QY	2521	GGGCTCGGCCCTAACCCAGGAGATTCGCCGTGAGAGAACTTTTAACTGCTGAAAGGAAGCA	2580
Db	2521	GGGCTCGGCCCTAACCCAGGAGATTCGCCGTGAGAGAACTTTTAACTGCTGAAAGGAAGCA	2580
QY	2581	CAGATGATTAAGCCAGGCCAACTGCACCAACGAACTGTACATGATGATGAAGGAGCTGTG	2640
Db	2581	CAGATGATTAAGCCAGGCCAACTGCACCAACGAACTGTACATGATGATGAAGGAGCTGTG	2640
QY	2641	GCATGCATGTCCTTCCCAAGACCAACGTTCAAGACATGTGTGAAGAACTTGGATCGAAT	2700
Db	2641	GCATGCATGTCCTTCCCAAGACCAACGTTCAAGACATGTGTGAAGAACTTGGATCGAAT	2700
QY	2701	TCTCACTCTCAACCAATGAGGAATACTTGGACCTCAGCCCAACTCTCGAACATATTC	2760
Db	2701	TCTCACTCTCAACCAATGAGGAATACTTGGACCTCAGCCCAACTCTCGAACATATTC	2760
QY	2761	ACCTTAGTTACCTGA	2775
Db	2761	AAGGTGCAAACTGA	2775

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RESULT 4
US-09-954-556-21
; Sequence 21, Application US/09954556
; Patent No. 6900053
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Scott Cooper
; TITLE OF INVENTION: ANTISENSE MODULATION OF FIBROBLAST GROWTH FACTOR RECEPTOR 2 EXPRESSION
; FILE REFERENCE: RTS-0250
; CURRENT APPLICATION NUMBER: US/09/954,556
; CURRENT FILING DATE: 2001-09-14
; NUMBER OF SEQ ID NOS: 108
; SEQ ID NO 21
; LENGTH: 2826
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (419)...(2725)
US-09-954-556-21

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Query Match	87.7%;	Score 2723.4;	DB 3;	Length 2826;
Best Local Similarity	99.9%;	Pred. No. 0;		
Matches 2724;	Conservative	0;	Mismatches 1;	Indels 0;
				Gaps 0
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Db	1	CCCGGAGCAAAATTGGTGTGAGGCAACGCAAGCTGATCTCTTCTTCTCGTCCC		60
QY	61	CAATTCGAGGCGACCCCGGCGCTCATGCGCGCTTCTTCGAGCCTGCGGTA		120
Db	61	CAATTCGAGGCGACCCCGGCGCTCATGCGCGCTTCTTCGAGCCTGCGGTA		120
QY	121	AGCCCGGAGGCTTGGCCGCCCGCGAAGACCCAAAGACCACTCTTCTGCGTTTGAGATTGC		180
Db	121	AGCCCGGAGGCTTGGCCGCCCGCGAAGACCCAAAGACCACTCTTCTGCGTTTGAGATTGC		180

QY	181	TCGCCGCA	CCCCGGGCTCGTCGGTTTCTCA	TCGCCGCA	CCGAGCGGGGACAA	C	240
Db	181	TCGCCGCA	CCCCGGGCTCGTCGGTTTCTCA	TCGCCGCA	CCGAGCGGGGACAA	C	240
QY	241	ACAGGTGCGGAGAGAGCGTTGCCATT	CAATTAAGTGA	CTGACAGCAG	CGCAGCGCTCGATT		300
Db	241	ACAGGTGCGGAGAGAGCGTTGCCATT	CAATTAAGTGA	CTGACAGCAG	CGCAGCGCTCGATT		300
QY	301	CCTGAGCCCA	CCGAGCTGAA	GGCATTGCGCGTAGTCCAT	CCCGTAGAGGAGATGTGCA	360	
Db	301	CCTGAGCCCA	CCGAGCTGAA	GGCATTGCGCGTAGTCCAT	CCCGTAGAGGAGATGTGCA	360	
QY	361	GATGGAGTTAA	CGTCCACAT	TGGAAATATGAA	AGACCGGGGAA	TTGGTACCGTTAACAT	420
Db	361	GATGGAGTTAA	CGTCCACAT	TGGAAATATGAA	AGACCGGGGAA	TTGGTACCGTTAACAT	420
QY	421	GGTGAGCTGGGGGTGGTTT	CATCTCGCGTGTGTA	GCATGACAA	CTTGTCCCTGGC	480	
Db	421	GGTGAGCTGGGGGTGGTTT	CATCTCGCGTGTGTA	GCATGACAA	CTTGTCCCTGGC	480	
QY	481	CCGGCCCTCTT	CAGTTTAA	GTGAGATACCA	ATTAGAGCCAGAA	AGCCAAACCA	540
Db	481	CCGGCCCTCTT	CAGTTTAA	GTGAGATACCA	ATTAGAGCCAGAA	AGCCAAACCA	540
QY	541	ATACCAATCTCT	CAACCA	GAAGTGAAGTGGCTCCG	CAGGGGAGTCGCTA	AGATGGTGG	600
Db	541	ATACCAATCTCT	CAACCA	GAAGTGAAGTGGCTCCG	CAGGGGAGTCGCTA	AGATGGTGG	600
QY	601	CTGCGCTGTTAA	AGATGGCGCGCGT	GATCAGTTGAGCTA	AGGATGGGGTGCA	CTTGGGGCC	660
Db	601	CTGCGCTGTTAA	AGATGGCGCGCGT	GATCAGTTGAGCTA	AGGATGGGGTGCA	CTTGGGGCC	660
QY	661	CAACATATGACA	CAGTGCTTAT	TGGGAGATCTTGACA	TAAAGGCGCACACCT	TAGAGA	720
Db	661	CAACATATGACA	CAGTGCTTAT	TGGGAGATCTTGACA	TAAAGGCGCACACCT	TAGAGA	720
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Db	721	CTCGGCGCTT	ATGCTGTTACTGCCAGTAGAGA	CTGTGACAGTGA	MACTTGGTATTTAT	780	
QY	781	GATGAATGTC	CAGATGTCATCTCA	TCGGAGATGATAGATGAGTGA	CA	CCGATGGTGGGA	840
Db	781	GATGAATGTC	CAGATGTCATCTCA	TCGGAGATGATAGATGAGTGA	CA	CCGATGGTGGGA	840
QY	841	AGATTTTGT	CAGTGAACA	GTTAACACAGAGACACAT	ACTGAGCAACACAGAAA	900	
Db	841	AGATTTTGT	CAGTGAACA	GTTAACACAGAGACACAT	ACTGAGCAACACAGAAA	900	
QY	901	GATGAAAA	GGCGCTCA	TGCTGTGTCGCGCCCA	CACTGTCAAGTTTCTGCTGCCAGC	960	
Db	901	GATGAAAA	GGCGCTCA	TGCTGTGTCGCGCCCA	CACTGTCAAGTTTCTGCTGCCAGC	960	
QY	961	CGGGGGGAA	CCCAATGCCAAC	CAATGCGGTGGCTGAAAA	CGGGAAGAGATT	TAA	1020
Db	961	CGGGGGGAA	CCCAATGCCAAC	CAATGCGGTGGCTGAAAA	CGGGAAGAGATT	TAA	1020
QY	1021	GCATGCGATT	TGAGGCTAC	AGATGCAAA	CCAGCAGCTGAGGCTCAT	TATGAGAAAGT	1080
Db	1021	GCATGCGATT	TGAGGCTAC	AGATGCAAA	CCAGCAGCTGAGGCTCAT	TATGAGAAAGT	1080
QY	1081	GGTCCCAT	CTGA	CAAGGAAATTA	TACCTGTGTATGAGATGAT	ACGGGTCCATCA	1140
Db	1081	GGTCCCAT	CTGA	CAAGGAAATTA	TACCTGTGTATGAGATGAT	ACGGGTCCATCA	1140
QY	1141	TCACACGTA	CCACTG	GATGTTTGGACGAT	CGCTCA	CGGCCCATCTC	1200
Db	1141	TCACACGTA	CCACTG	GATGTTTGGACGAT	CGCTCA	CGGCCCATCTC	1200
QY	1201	ACTGCGGCAAA	TGCTGCA	CACTGCTGAGAGAC	AGTGAAGTTGTCTGCA	AGTTTA	1260
Db	1201	ACTGCGGCAAA	TGCTGCA	CACTGCTGAGAGAC	AGTGAAGTTGTCTGCA	AGTTTA	1260
QY	1261	CAGTATG	CCGACCCCA	ATTCAGTGA	TCAAGCAGTGA	AAAAAAGAA	1320
Db	1261	CAGTATG	CCGACCCCA	ATTCAGTGA	TCAAGCAGTGA	AAAAAAGAA	1320

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 Db 1321 CCGGCCCCAGCGGCTGCTTACCTCAAGGTTCTCAAGCACTCGGGGATTAATAGTCCAA 1380
 Qy 1381 TGAAGAAAGTCTGCTCTGTTCATGTGACCGAGCGGAGATGTGGGAAATATATGTAA 1440
 Db 1381 TGAAGAAAGTCTGCTCTGTTCATGTGACCGAGCGGAGATGTGGGAAATATATGTAA 1440
 Qy 1441 GGTCTCAATTAATATAGGAGGAGGCAACAGTCTGCTGCTCACTGTCTGCAAAACA 1500
 Db 1441 GGTCTCAATTAATATAGGAGGAGGCAACAGTCTGCTGCTCACTGTCTGCAAAACA 1500
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 Db 1501 GCAAGCGCTGGAAGAAAAGAGATTACAGCTTCCCACTACTGAGATAGCCAT 1560
 Qy 1561 TTAATGATAGGGGTCTTCTTAATCCCTGTATGTGTAAAGTCACTCTGTGCGAAT 1620
 Db 1561 TTAATGATAGGGGTCTTCTTAATCCCTGTATGTGTAAAGTCACTCTGTGCGAAT 1620
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 Db 1621 GAAGAACAGCAAGAAAGCAGACTTCAGCAGCGCGCTGTGCAAGAGTGAACAA 1680
 Qy 1681 ACCTATCCCTCTCGAGAGAGGTAACAGTTCCGCTGAGTCCAGTCTCAATGAATC 1740
 Db 1681 ACCTATCCCTCTCGAGAGAGGTAACAGTTCCGCTGAGTCCAGTCTCAATGAATC 1740
 Qy 1741 CAACACCCCGCTGTGAGTAACACAGCCCTCTCTTCAACCGCAGACACCCCATGCT 1800
 Db 1741 CAACACCCCGCTGTGAGTAACACAGCCCTCTCTTCAACCGCAGACACCCCATGCT 1800
 Qy 1801 GGAAGGGGTCTCCAGATGAACTTCCAGAGAACCCAAATGGAAGTTTCAAGAGATA 1860
 Db 1801 GGAAGGGGTCTCCAGATGAACTTCCAGAGAACCCAAATGGAAGTTTCAAGAGATA 1860
 Qy 1861 GCTGACACTGGGAGAGCCCTGGGAGAGAGGTGCTTGGGCAAGTGTCAATGGCGAAGC 1920
 Db 1861 GCTGACACTGGGAGAGCCCTGGGAGAGAGGTGCTTGGGCAAGTGTCAATGGCGAAGC 1920
 Qy 1921 AGTGGGAATTGACAAAGACCAAGCCCAAGAGGCGGTCACTGTGCGCTGAAAGTGTGA 1980
 Db 1921 AGTGGGAATTGACAAAGACCAAGCCCAAGAGGCGGTCACTGTGCGCTGAAAGTGTGA 1980
 Qy 1981 AGATGATGCCACAGAGAAAGACCTTCTGATCTGTGTCAAGATGAGATGAAGAT 2040
 Db 1981 AGATGATGCCACAGAGAAAGACCTTCTGATCTGTGTGTCAAGATGAGATGAAGAT 2040
 Qy 2041 GATTGGGAAACACAAAGATATCAATAATCTTCTTGAAGCTGCAACAGATGGGCTCT 2100
 Db 2041 GATTGGGAAACACAAAGATATCAATAATCTTCTTGAAGCTGCAACAGATGGGCTCT 2100
 Qy 2101 CTATGTCATAGTGAATGCTCTTAAGGCAACTTCGAGAACTCTCCGAGCCCGAG 2160
 Db 2101 CTATGTCATAGTGAATGCTCTTAAGGCAACTTCGAGAACTCTCCGAGCCCGAG 2160
 Qy 2161 GCCACCGGAGATGAGACTCTCTATGACATTAACCGGTCTCTGAGAGAGAGATGACTT 2220
 Db 2161 GCCACCGGAGATGAGACTCTCTATGACATTAACCGGTCTCTGAGAGAGAGATGACTT 2220
 Qy 2221 CAAGAGCTTGTGTCATGACCTACAGCTGCGCAGAGAGATGAGATGCTTCCCA 2280
 Db 2221 CAAGAGCTTGTGTCATGACCTACAGCTGCGCAGAGAGATGAGATGCTTCCCA 2280
 Qy 2281 AAAATGATTCATGAGATTTAGAGCCAGAAATGTTTGTGTAACAGAAAACAATGTGAT 2340
 Db 2281 AAAATGATTCATGAGATTTAGAGCCAGAAATGTTTGTGTAACAGAAAACAATGTGAT 2340
 Qy 2341 GAAATAGCAGACTTTGAGCTCGCAGAGATCAACATATGACTATTAACAAAAGAC 2400
 Db 2341 GAAATAGCAGACTTTGAGCTCGCAGAGATCAACATATGACTATTAACAAAAGAC 2400

Db 2341 GAAATAGCAGACTTTGAGCTCGCAGAGATCAACATATGACTATTAACAAAAGAC 2400
 Qy 2401 CACCAATGGGCGGCTTCAAGTGAAGTGGCTCCAGAGACCTGTTGATGAGATATA 2460
 Db 2401 CACCAATGGGCGGCTTCAAGTGAAGTGGCTCCAGAGACCTGTTGATGAGATATA 2460
 Qy 2461 CACTCATCAGAGATGATGTGCTCTCGGGGTGTAATGTGGAGATCTTCACTTAAAG 2520
 Db 2461 CACTCATCAGAGATGATGTGCTCTCGGGGTGTAATGTGGAGATCTTCACTTAAAG 2520
 Qy 2521 GGGCTGCGCTTACCCAGGATTCCTGTGAGAACTTTTAAGCTCTGAAGAGAGCA 2580
 Db 2521 GGGCTGCGCTTACCCAGGATTCCTGTGAGAACTTTTAAGCTCTGAAGAGAGCA 2580
 Qy 2581 CAGATGATGATGAGCCAGCCCACTGACCAACGATCTGATGATGAGGAGCTGTTG 2640
 Db 2581 CAGATGATGATGAGCCAGCCCACTGACCAACGATCTGATGATGAGGAGCTGTTG 2640
 Qy 2641 GCATGAGTGCCTTCCCAAGAGACCAAGTTCAGAGAGTGTGAGAACTTGTGATGAT 2700
 Db 2641 GCATGAGTGCCTTCCCAAGAGACCAAGTTCAGAGAGTGTGAGAACTTGTGATGAT 2700
 Qy 2701 TCTCACTCTCAACCAATGAGGAA 2725
 Db 2701 TCTCACTCTCAACCAATGAGTAA 2725

RESULT 5
 US-09-954-556-19
 ; Sequence 19, Application US/09954556
 ; Patent No. 690053
 ; GENERAL INFORMATION:
 ; APPLICANT: Brett P. Morita
 ; APPLICANT: Susan W. Freiler
 ; APPLICANT: Scott Cooper
 ; TITLE OF INVENTION: ANTISENSE MODULATION OF FIBROBLAST GROWTH FACTOR RECEPTOR 2 EXPRESSION
 ; FILE REFERENCE: RTS-0250
 ; CURRENT APPLICATION NUMBER: US/09/954,556
 ; NUMBER OF SEQ ID NOS: 108
 ; SEQ ID NO 19
 ; LENGTH: 2868
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (419)...(2734)
 US-09-954-556-19

Query Match 87.6%; Score 2722; DB 3; Length 2868;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 2722; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 CCGGAGCAAGTGTGAGAGGCAACGAGCTGAGTCTTCTCTCTCTGTTCCC 60
 Db 1 CCGGAGCAAGTGTGAGAGGCAACGAGCTGAGTCTTCTCTCTCTGTTCCC 60
 Qy 61 CAATCCGAGGAGGAGCCCGGCGGTGATGCGCTCTCCGACAGCTGGGATACGCTGA 120
 Db 61 CAATCCGAGGAGGAGCCCGGCGGTGATGCGCTCTCCGACAGCTGGGATACGCTGA 120
 Qy 121 AGCCCGGAGGCTTGGCGCCGCGGAGAACCCAGAGACACTCTTGTGAGTGTG 180
 Db 121 AGCCCGGAGGCTTGGCGCCGCGGAGAACCCAGAGACACTCTTGTGAGTGTG 180
 Qy 181 TCCCGCAACCCCGGCGTGTGCTTCTCATCCGACCCAGCGCGGCGCGGAGCAAC 240
 Db 181 TCCCGCAACCCCGGCGTGTGCTTCTCATCCGACCCAGCGCGGCGCGGAGCAAC 240
 Qy 241 ACAAGTGCAGAGAGGCTTGCATTCAGTGACTGAGAGAGAGAGAGAGAGAGAGAG 300
 Db 241 ACAAGTGCAGAGAGGCTTGCATTCAGTGACTGAGAGAGAGAGAGAGAGAGAGAG 300

QY 301 CCTGAGCCACCGCAGCTGAGAGGCATTGCGCGTATGTCATGCCCCGTAGAGGAATGTGCA 360
DB 301 CCTGAGCCACCGCAGCTGAGAGGCATTGCGCGTATGTCATGCCCCGTAGAGGAATGTGCA 360
QY 361 GATTGGATTAAAGTCCACATGAGATATGGAAGAGGACCGGGGATTTGGATACGGTAACAT 420
DB 361 GATTGGATTAAAGTCCACATGAGATATGGAAGAGGACCGGGGATTTGGATACGGTAACAT 420
QY 421 GGTCAAGTGGGGTCTGTTTCATCTGCTGTGTGTGTCAACATGCAACTTGTCTCTGTGC 480
DB 421 GGTCAAGTGGGGTCTGTTTCATCTGCTGTGTGTGTCAACATGCAACTTGTCTCTGTGC 480
QY 481 CCGGCGCTCTCTCAAGTTTATGTTAGAGATACCATTAAGCCGAAAGACCCAAACCA 540
DB 481 CCGGCGCTCTCTCAAGTTTATGTTAGAGATACCATTAAGCCGAAAGACCCAAACCA 540
QY 541 ATACCAAAATCTCTCAACCAAGATGTAAGTGTGCGTGCAGAGGGAGTGTGCTAGAGGTGCG 600
DB 541 ATACCAAAATCTCTCAACCAAGATGTAAGTGTGCGTGCAGAGGGAGTGTGCTAGAGGTGCG 600
QY 601 CTGCTCTGTGAAGAATGCCGCGTGTATCAGTTGGACTTAAGATGGGGTCACTTGGGGCC 660
DB 601 CTGCTCTGTGAAGAATGCCGCGTGTATCAGTTGGACTTAAGATGGGGTCACTTGGGGCC 660
QY 661 CAACAATAGGACAGTGTCTTATTTGGGGAGTACTTGCAGATTAAGGGCGCCACACTTAGA 720
DB 661 CAACAATAGGACAGTGTCTTATTTGGGGAGTACTTGCAGATTAAGGGCGCCACACTTAGA 720
QY 721 CTCGCGCTCTATGCTTGTATCTGCCAGTGGAGCTGTAGACAGTGAACCTTGGTACTTCA 780
DB 721 CTCGCGCTCTATGCTTGTATCTGCCAGTGGAGCTGTAGACAGTGAACCTTGGTACTTCA 780
QY 781 GGTGAATGTCAAGATGTCATCTCATCCGAGATGATGAGATGACACCGATGTGCGGA 840
DB 781 GGTGAATGTCAAGATGTCATCTCATCCGAGATGATGAGATGACACCGATGTGCGGA 840
QY 841 AGATTTTGTCAAGTGAACAAGTAAACAACAAGAGACCACTTAGACCAACAAGAAA 900
DB 841 AGATTTTGTCAAGTGAACAAGTAAACAACAAGAGACCACTTAGACCAACAAGAAA 900
QY 901 GATTGAAAAGCGGCTCATGCTGTGCTGCGCCAACTGTCAAGTTTGTGCTGCCACG 960
DB 901 GATTGAAAAGCGGCTCATGCTGTGCTGCGCCAACTGTCAAGTTTGTGCTGCCACG 960
QY 961 CCGGGGGAAACCAATGCGCAACATGCGGTGGCTGAAGAAACGGGAGAGATTAAAGCAGA 1020
DB 961 CCGGGGGAAACCAATGCGCAACATGCGGTGGCTGAAGAAACGGGAGAGATTAAAGCAGA 1020
QY 1021 GCATGCGATTGGAGGCTACAAAGTACGAAACCAAGCACTGAGGCTCATTAATGAAAGTGT 1080
DB 1021 GCATGCGATTGGAGGCTACAAAGTACGAAACCAAGCACTGAGGCTCATTAATGAAAGTGT 1080
QY 1081 GGTCCCATCTGACAAAGGAAATTTATCTGTGTAGTGAATGAATACGGGTCCATCA 1140
DB 1081 GGTCCCATCTGACAAAGGAAATTTATCTGTGTAGTGAATGAATACGGGTCCATCA 1140
QY 1141 TCACAGTACCACTGTGATGTTGTGAGCGATGCGCTCACCGGCCCATCTCCAAAGCGGG 1200
DB 1141 TCACAGTACCACTGTGATGTTGTGAGCGATGCGCTCACCGGCCCATCTCCAAAGCGGG 1200
QY 1201 ACTGCGCGCAATGCTCTCCACAGTGTGCGAGGAGAGTGAAGTGTGTCTGCAAGGTTTA 1260
DB 1201 ACTGCGCGCAATGCTCTCCACAGTGTGCGAGGAGAGTGAAGTGTGTCTGCAAGGTTTA 1260
QY 1261 CAGTGAATGCCAGGCCCATCTCAGTGGATCAAGCACTGAGAAAGAAAGACGGCAGTAAATA 1320
DB 1261 CAGTGAATGCCAGGCCCATCTCAGTGGATCAAGCACTGAGAAAGAAAGACGGCAGTAAATA 1320
QY 1321 CCGGCGCGCAGCGGGCTGCTTACCTCAAGGTTTCTCAAGCACTCGGGGATTAATAATGTTCAA 1380
DB 1321 CCGGCGCGCAGCGGGCTGCTTACCTCAAGGTTTCTCAAGCACTCGGGGATTAATAATGTTCAA 1380
QY 1381 TGCAGAAATGCTGCTGTTCATATGACCGAGGCGGATGCTGGGAAATATATATGTAA 1440

DB 1381 TGCAGAAATGCTGCTGTTCATATGACCGAGGCGGATGCTGGGAAATATATATGTAA 1440
QY 1441 GGTCTCCAAATATATAGGGCAGGCCAACCACTGTGCTGTGCTCACTGTCTGCGCAAAACA 1500
DB 1441 GGTCTCCAAATATATAGGGCAGGCCAACCACTGTGCTGTGCTCACTGTCTGCGCAAAACA 1500
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DB 1501 GCAGCGCTTGGAAAGAAAGAGATTAACAGCTTCCCGACACTACCTGAGATAGCCAT 1560
QY 1561 TTACTGCAATAGGGGCTCTTAAATGCTGTATGTTGTGTAAACAGTCACTGTGTGCGAAT 1620
DB 1561 TTACTGCAATAGGGGCTCTTAAATGCTGTATGTTGTGTAAACAGTCACTGTGTGCGAAT 1620
QY 1621 GAAAGAACAGCAAGAAAGCAAGTCAAGTCAAGCAGCCGCTGTGCAAGCTGACCA 1680
DB 1621 GAAAGAACAGCAAGAAAGCAAGTCAAGTCAAGCAGCCGCTGTGCAAGCTGACCA 1680
QY 1681 AGGTATCCCCCTGCGGAGACAGGTAAACGTTTCCGCTGAGTCCAGCTCTCATGAACTC 1740
DB 1681 AGGTATCCCCCTGCGGAGACAGGTAAACGTTTCCGCTGAGTCCAGCTCTCATGAACTC 1740
QY 1741 CAACACCCCGCTGTGAGGATTAACAAGCCTCTCTTCAACGCGCAGACACCCCATGCT 1800
DB 1741 CAACACCCCGCTGTGAGGATTAACAAGCCTCTCTTCAACGCGCAGACACCCCATGCT 1800
QY 1801 GGCAGGGGTCTTCGAGTATGAACCTTCCAGAGAACCAAAATGGGATTTCCAAAGATTA 1860
DB 1801 GGCAGGGGTCTTCGAGTATGAACCTTCCAGAGAACCAAAATGGGATTTCCAAAGATTA 1860
QY 1861 GCTGACACTGGGCAAGCCCTGSGGAAAGTGTGCTTGGGCAAGTGTGATGGCGGAAGC 1920
DB 1861 GCTGACACTGGGCAAGCCCTGSGGAAAGTGTGCTTGGGCAAGTGTGATGGCGGAAGC 1920
QY 1921 AGTGGAAATTTGCAAAAGCAAGCCCAAGAGGCGGTCAACGCTGAGCCGTGAAGATGTGA 1980
DB 1921 AGTGGAAATTTGCAAAAGCAAGCCCAAGAGGCGGTCAACGCTGAGCCGTGAAGATGTGA 1980
QY 1981 AGATGATGCAAGAGAAAGACCTTTCTGATCTGTGTGCAAGATGAGATATGAAGAT 2040
DB 1981 AGATGATGCAAGAGAAAGACCTTTCTGATCTGTGTGCAAGATGAGATATGAAGAT 2040
QY 2041 GATTGGGAAACCAAGAAATATATTAATCTTGTGAGCTGSCACACAGATGGGCTCT 2100
DB 2041 GATTGGGAAACCAAGAAATATATTAATCTTGTGAGCTGSCACACAGATGGGCTCT 2100
QY 2101 CTATGCTATGATGATGCTCTTAAAGGCAACCTCCGAGAAATCTTCCAGCGGAG 2160
DB 2101 CTATGCTATGATGATGCTCTTAAAGGCAACCTCCGAGAAATCTTCCAGCGGAG 2160
QY 2161 GCCACCCGGGATGAGTACTCTTATGACATTAACCGTGTCTTGGAGCAATGACTT 2220
DB 2161 GCCACCCGGGATGAGTACTCTTATGACATTAACCGTGTCTTGGAGCAATGACTT 2220
QY 2221 CAAGGACTGTGTGATGACCTTACAGCTGCGCAGACGAGTGAATCTTGGCTTCCA 2280
DB 2221 CAAGGACTGTGTGATGACCTTACAGCTGCGCAGACGAGTGAATCTTGGCTTCCA 2280
QY 2281 AAAATGTATTCATCGAATTTTAGCAGCCGAAATGTTTGTGTAAGAAACAATGTGAT 2340
DB 2281 AAAATGTATTCATCGAATTTTAGCAGCCGAAATGTTTGTGTAAGAAACAATGTGAT 2340
QY 2341 GAAATATAGCAGACTTTGACTGCGCAGAGATTAACAATATATGACTATTAACAAAAGAC 2400
DB 2341 GAAATATAGCAGACTTTGACTGCGCAGAGATTAACAATATATGACTATTAACAAAAGAC 2400
QY 2401 CACCAATGGCGGCTTCCAGTAAAGTGAATGCTCCAGAAAGCCGTGTGATGAGATATA 2460
DB 2401 CACCAATGGCGGCTTCCAGTAAAGTGAATGCTCCAGAAAGCCGTGTGATGAGATATA 2460
QY 2461 CACTCATCAGAGTATGTGTCTTCCGGGGTGTAAATGTGAGGATCTTCACTTTAGG 2520

Accession	Sequence	Length
Db	CACCTCAGAGTATGTCTGCTCTTGGGGGTGTATGTGGAGATCTTCACTTTAGG	2520
Qy	GGGCTCGCCCTACCAAGGATTCCTGTGAGGAACTTTTAACTGTCTGAAGAGACA	2580
Db	GGGCTCGCCCTACCAAGGATTCCTGTGAGGAACTTTTAACTGTCTGAAGAGACA	2580
Qy	CAGATGGATTAAGCAGCCAACTGCAACAAAGAACTGACATGTATGATGAGGACTGTG	2640
Db	CAGATGGATTAAGCAGCCAACTGCAACAAAGAACTGACATGTATGATGAGGACTGTG	2640
Qy	GCATGCAGTGCTCTCCAGAGACCAACTTTCAAGCACTTGTATGAGAACTTGCATCGAAT	2700
Db	GCATGCAGTGCTCTCCAGAGACCAACTTTCAAGCACTTGTATGAGAACTTGCATCGAAT	2700
Qy	TCTCACTCTCAACCAATGAG	2722
Db	TCTCACTCTCAACCAATGAG	2722

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RESULT 6
US-09-954-556-18
; Sequence 18, Application US/09954556
; Patent No. 6900053
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Preler
; APPLICANT: Scott Cooper
; TITLE OF INVENTION: ANTISENSE MODULATION OF FIBROBLAST GROWTH FACTOR RECEPTOR 2 EXPRESSION
; FILE REFERENCE: RTS-0250
; CURRENT APPLICATION NUMBER: US/09/954,556
; CURRENT FILING DATE: 2001-09-14
; NUMBER OF SEQ ID NOS: 108
; SEQ ID NO: 18
; LENGTH: 2941
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURES:
; NAME/KEY: CDS
; LOCATION: (419)...(2878)
US-09-954-556-18

Query Match      87.6%; Score 2722; DB 3; Length 2941;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2722; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1      CCCGAGCAAGTTTGATGAGCGCAAGCGTGAAGTCTTCTCTCTGTTCCC 60
DB      1      CCCGAGCAAGTTTGATGAGCGCAAGCGTGAAGTCTTCTCTCTGTTCCC 60

QY      61      CAAATCCGAGGGAGCCCGCGGGCGTCATGAGCGCTCCTCCGAGCTTGAGCGGTGA 120
DB      61      CAAATCCGAGGGAGCCCGCGGGCGTCATGAGCGCTCCTCCTCGAGCTTGAGCGGTGA 120

QY      121     AGCCCGGAGGCTTTGCGCGCGCGAAGACCCAAAGACCACTTTCTGCGTTGAGATTGC 180
DB      121     AGCCCGGAGGCTTTGCGCGCGCGAAGACCCAAAGACCACTTTCTGCGTTGAGATTGC 180

QY      181     TCCCCCGCAACCCCCGGGCTCGTTCGTTTCTCATCCCGACCCAGCGGGCGGGGAGCAAC 240
DB      181     TCCCCCGCAACCCCCGGGCTCGTTCGTTTCTCATCCCGACCCAGCGGGCGGGGAGCAAC 240

QY      241     ACAGGTGCGGAGGAGCGTTGCCATTCAAGTGACTGCGAGCAGACGCGAGCGCTCGGTT 300
DB      241     ACAGGTGCGGAGGAGCGTTGCCATTCAAGTGACTGCGAGCAGACGCGAGCGCTCGGTT 300

QY      301     CCTGAGCCACCGACGCTGAAGGCAATTGCGCGTAGTCCATGCCGTAGAGGAAGTGTCA 360
DB      301     CCTGAGCCACCGACGCTGAAGGCAATTGCGCGTAGTCCATGCCGTAGAGGAAGTGTCA 360

QY      361     GATGGAGTTAATCGTCCATATGAGATATGAAAGAGACCGGGGAGTTGTAACGTAAACAT 420
DB      361     GATGGAGTTAATCGTCCATATGAGATATGAAAGAGACCGGGGAGTTGTAACGTAAACAT 420

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QY	421	GGTCAAGCTGGGGGTGTTTCATCTGCTGTGTGTGTGTCACTATGGCAACCTTGTCCCTGGC	480
Db	421	GGTCAGCTGGGGGTGTTTCATCTGCTGTGTGTGTGTCACTATGGCAACCTTGTCCCTGGC	480
QY	481	CCGGCCCTCCCTCAGTTTAGTGGATACCACTTAGAGCCAGAAAGGCCAACCAACA	540
Db	481	CCGGCCCTCCCTCAGTTTAGTGGATACCACTTAGAGCCAGAAAGGCCAACCAACA	540
QY	541	ATACCAATCTCTTCACAGAAAGTGTACGTGTGCTGCCAGAGGGAGTGTGTAGAGTGC	600
Db	541	ATACCAATCTCTTCACAGAAAGTGTACGTGTGCTGCCAGAGGGAGTGTGTAGAGTGC	600
QY	601	CTGCTCTGTGAAGATGCTCCCGCTGATCATGTTGAGCTTAAGATGTGGGTGCATTGGGGCC	660
Db	601	CTGCTCTGTGAAGATGCTCCCGCTGATCATGTTGAGCTTAAGATGTGGGTGCATTGGGGCC	660
QY	661	CAACAATATGACATGTGCTTATGTGGAGTACTTGCAATTAAGGGGCGCCACACTTAAGA	720
Db	661	CAACAATATGACATGTGCTTATGTGGAGTACTTGCAATTAAGGGGCGCCACACTTAAGA	720
QY	721	CTCCGGCCTCATGCTCTGTACTGCCAGTAGAGACTGTAGACATGTGAACTTGTGATCTTCAT	780
Db	721	CTCCGGCCTCATGCTCTGTACTGCCAGTAGAGACTGTAGACATGTGAACTTGTGATCTTCAT	780
QY	781	GGTAGATGTCAAGATGCCATCTCATTCGGAGATGATGAGATGTACACCGATGTGTGCGA	840
Db	781	GGTAGATGTCAAGATGCCATCTCATTCGGAGATGATGAGATGTACACCGATGTGTGCGA	840
QY	841	AGATTTTGTCAGTATGAGAACAGTACCAAGAAGGCAACATCTGAGCCAAACACAGAAA	900
Db	841	AGATTTTGTCAGTATGAGAACAGTACCAAGAAGGCAACATCTGAGCCAAACACAGAAA	900
QY	901	GATGGAAAAGGGGCTCATGCTGTGCTGTGCGGCCAAACATGTCAAGTTTGCTGTGCCAGC	960
Db	901	GATGGAAAAGGGGCTCATGCTGTGCTGTGCGGCCAAACATGTCAAGTTTGCTGTGCCAGC	960
QY	961	CGGGGGGAAACCCAAATGCCAACATGTGGGTGGCTGAAAAACGGGAAGAGTTTAAACAGAA	1020
Db	961	CGGGGGGAAACCCAAATGCCAACATGTGGGTGGCTGAAAAACGGGAAGAGTTTAAACAGAA	1020
QY	1021	GCATTCGATTTGAGAGCTTACAAAGTATCGAAACCGACTTGAAGCTCATTTATGAAATGT	1080
Db	1021	GCATTCGATTTGAGAGCTTACAAAGTATCGAAACCGACTTGAAGCTCATTTATGAAATGT	1080
QY	1081	GGTCCCATCTGACAAAGGAAATTTATCTGTGTATGTGAAGATGAAATACGGGTTCATCAA	1140
Db	1081	GGTCCCATCTGACAAAGGAAATTTATCTGTGTATGTGAAGATGAAATACGGGTTCATCAA	1140
QY	1141	TCACAAGTACCACTGTGATGTTGTGAGCGATGTGCTCACCGGCCCATCTCCAAAGCCGG	1200
Db	1141	TCACAAGTACCACTGTGATGTTGTGAGCGATGTGCTCACCGGCCCATCTCCAAAGCCGG	1200
QY	1201	ACTGCGGCGCAATGCTTCCACATGTGTGCGAGAGACGTAGAGTTTGTCTGCAAGTTTAA	1260
Db	1201	ACTGCGGCGCAATGCTTCCACATGTGTGCGAGAGAGTGTAGAGTTTGTCTGCAAGTTTAA	1260
QY	1261	CAGTAGTGCCCAAGGCCCAACATCAAGTGTATCAACACGTGTGAAAAGAACGCGAGTAATA	1320
Db	1261	CAGTAGTGCCCAAGGCCCAACATCAAGTGTATCAACACGTGTGAAAAGAACGCGAGTAATA	1320
QY	1321	CGGGCCCGACCGGGCTGCTCTACCTCAAGGTTCTTCACAGCACTCGGGGATTAATAGTTCCAA	1380
Db	1321	CGGGCCCGACCGGGCTGCTCTACCTCAAGGTTCTTCACAGCACTCGGGGATTAATAGTTCCAA	1380
QY	1381	TGCAGAAAGTGTGCTCTGTTCAATGTGTACCGAGGCGGATGTGTGGGAAATATATATGTAA	1440
Db	1381	TGCAGAAAGTGTGCTCTGTTCAATGTGTACCGAGGCGGATGTGTGGGAAATATATATGTAA	1440
QY	1441	GSTCTCCAAATATATATAGGGGAGGCGCAACATGTGCTGAGGTCACTGTCTGTCCCAAAACA	1500
Db	1441	GSTCTCCAAATATATATAGGGGAGGCGCAACATGTGCTGAGGTCACTGTCTGTCCCAAAACA	1500
QY	1501	GCAAGCGCTGTGAAGAAAAAGAGATTACAGTTCTCCAGACTTACCTGTGAGTATGCGAT	1560

Db 1501 GGAAGGCTTGAAGAGAAAGAGATACAGCTTCCAGACTACCTGAGATAGCCAT 1560
Qy 1561 TTACTGATAGAGGGTCTTCTTAATCGCTGTATGTGTATACAGTCATCTGTCCGAAT 1620
Db 1561 TTACTGATAGAGGGTCTTCTTAATCGCTGTATGTGTATACAGTCATCTGTCCGAAT 1620
Qy 1621 GAAAGACAGACCAAGAGCCAGACTTTCAGACGCCAGCCGGCTGTGCAAGAGTCACCA 1680
Db 1621 GAAAGACAGACCAAGAGCCAGACTTTCAGACGCCAGCCGGCTGTGCAAGAGTCACCA 1680
Qy 1681 AGGTATCCCTGCGGAGACAGGTACAGTTTCGGTGTAGTCCAGCTCCCTCAAGATC 1740
Db 1681 AGGTATCCCTGCGGAGACAGGTACAGTTTCGGTGTAGTCCAGCTCCCTCAAGATC 1740
Qy 1741 CAACACCCCGCTGTGTAGATACCAACACGCTCTCTTCAACGCGCAGACCCCAATGCT 1800
Db 1741 CAACACCCCGCTGTGTAGATACCAACACGCTCTCTTCAACGCGCAGACCCCAATGCT 1800
Qy 1801 GGCAGGGGTCTCCGAGTATGAATTCAGAGACCCAAATGGAGATTTCAGAGATTA 1860
Db 1801 GGCAGGGGTCTCCGAGTATGAATTCAGAGACCCAAATGGAGATTTCAGAGATTA 1860
Qy 1861 GCTGACACTGGGCAACCCCTGGGAGAGAGGTTCCTTGGGCAAGTGTCAATGCGGAGC 1920
Db 1861 GCTGACACTGGGCAACCCCTGGGAGAGAGGTTCCTTGGGCAAGTGTCAATGCGGAGC 1920
Qy 1921 AGTGGAAATGACCAAGACCAAGCCCAAGAGCGGATCACCGTGGCCGTGAAGTGTGA 1980
Db 1921 AGTGGAAATGACCAAGACCAAGCCCAAGAGCGGATCACCGTGGCCGTGAAGTGTGA 1980
Qy 1981 AGATGATGCCACAGAGAAAGACCTTCTGTATCTGTGTCAAGATGTGAAGT 2040
Db 1981 AGATGATGCCACAGAGAAAGACCTTCTGTATCTGTGTCAAGATGTGAAGT 2040
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Db 2041 GATGGGAAACCAAGATATCATTAATCTTGTGAGCCTGACACAGATGGGCTCT 2100
Qy 2101 CTATGTCATAGTGAATATGCTCTTAAGGCACTTCAGAGATACCTCGAGCCCGAG 2160
Db 2101 CTATGTCATAGTGAATATGCTCTTAAGGCACTTCAGAGATACCTCGAGCCCGAG 2160
Qy 2161 GCCACCCGGAGTGAATCTCTATGACATTAACCGTGTCTCTGAGAGACATGACCTT 2220
Db 2161 GCCACCCGGAGTGAATCTCTATGACATTAACCGTGTCTCTGAGAGACATGACCTT 2220
Qy 2221 CAAGACTTGTGTGATGACCTTACAGCTGAGCGGACAGAGATGAGATGAGCTTCCCA 2280
Db 2221 CAAGACTTGTGTGATGACCTTACAGCTGAGCGGACAGAGATGAGATGAGCTTCCCA 2280
Qy 2281 AAAATGTATTCAGATGATTTAGACAGCCAGAAATGTTTGTGAACAGAAACATGTGAT 2340
Db 2281 AAAATGTATTCAGATGATTTAGACAGCCAGAAATGTTTGTGAACAGAAACATGTGAT 2340
Qy 2341 GAAATATGACAGACTTTGATGCTGCCAGAGATATCAACATATGACTATTAACAAAAGC 2400
Db 2341 GAAATATGACAGACTTTGATGCTGCCAGAGATATCAACATATGACTATTAACAAAAGC 2400
Qy 2401 CACCAATGGGCGGCTTCAGTCAAGTGAATGGCTCCAGAAAGCCCTGTTGATGAGATTA 2460
Db 2401 CACCAATGGGCGGCTTCAGTCAAGTGAATGGCTCCAGAAAGCCCTGTTGATGAGATTA 2460
Qy 2461 CACTCATCAGATGATGTGATCTTTCGGGATGTTAATGTGGAGATCTTCACTTTAG 2520
Db 2461 CACTCATCAGATGATGTGATCTTTCGGGATGTTAATGTGGAGATCTTCACTTTAG 2520
Qy 2521 GGGCTGCGCTTACCCAGAGATTCCTGAGAGAACTTTTAACTGTGAAGAGAC 2580
Db 2521 GGGCTGCGCTTACCCAGAGATTCCTGAGAGAACTTTTAACTGTGAAGAGAC 2580
Qy 2581 CAGATGATTAACGAGCCAACTGACCAAGAACTGATCATGATGAGGAGCTGTTG 2640
Db 2581 CAGATGATTAACGAGCCAACTGACCAAGAACTGATCATGATGAGGAGCTGTTG 2640

Db 2581 CAGATGATTAACGAGCCAACTGACCAAGAACTGATCATGATGAGGAGCTGTTG 2640
Qy 2641 GCATCAGTGCCTTCCAGAGACCAAGCTTCAAGCATTTGTAAGAACTTGGATCGAAT 2700
Db 2641 GCATCAGTGCCTTCCAGAGACCAAGCTTCAAGCATTTGTAAGAACTTGGATCGAAT 2700
Qy 2701 TCTCACTCTCAACCAATGAG 2722
Db 2701 TCTCACTCTCAACCAATGAG 2722

RESULT 7
US-08-451-822A-15
; Sequence 15, Application US/08451822A
; Patent No. 586388
; GENERAL INFORMATION:
; APPLICANT: Dione, Craig A
; APPLICANT: Crumley, Greg
; APPLICANT: Jaye, Michael C
; APPLICANT: Schlesinger, Joseph
; TITLE OF INVENTION: Fibroblast Growth Factor Receptors
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rhone-Poulenc Rorer Legal Department
; STREET: 500 Arcola Road
; CITY: Collegeville
; STATE: PA
; COUNTRY: USA
; ZIP: 19426
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/451,822A
FILING DATE: 26-MAY-1995
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/323,430
FILING DATE: 14-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/934,372
FILING DATE: 21-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/549,587
FILING DATE: 06-JUL-1990
ATTORNEY/AGENT INFORMATION:
NAME: Savitzky, Martin
REGISTRATION NUMBER: 29,699
REFERENCE/DOCKET NUMBER: A0496E
TELECOMMUNICATION INFORMATION:
TELEPHONE: (610) 454-3816
TELEFAX: (610) 454-3808
INFORMATION FOR SEO ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 3416 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-451-822A-15

Query Match 87.4%; Score 2714.2; DB 2; Length 3416;
Best Local Similarity 97.1%; Pred. No. 0;
Matches 2790; Conservative 0; Mismatches 68; Indels 15; Gaps 2;

Qy 240 CACAGGTGCGGAGAGAGCTTGCATTAAGTGAAGTGAAGAGCGGAGCGCTCGGT 299
Db 2 CCGAGGTGCGGAGAGAGCTTGCATTAAGTGAAGTGAAGAGCGGAGCGCTCGGT 61
Qy 300 TCTGAGCCCAAGAGCTGAAGGATTCGCGGTAGTCCATGCCGTAGAGAGATGTGC 359
Db 300 TCTGAGCCCAAGAGCTGAAGGATTCGCGGTAGTCCATGCCGTAGAGAGATGTGC 359

Db 62 TCCGAGCCCAACCGCAGCTGAGGCAATTGCGCGTATGTCATGCCCGGTAGAGAGATGTGC 121
Qy 360 AGATGGATTAAGTCCATATGAGATATGGAAGAGACCGGGATTTGGTACCGTAAACA 419
Db 122 AGATGGATTAAGTCCATATGAGATATGGAAGAGACCGGGATTTGGTACCGTAAACA 181
Qy 420 TGGTCAAGCTGGGGGTGCTTATCTGCTGGTGGTGGTCAACATGAGCAACCTTGGCTTGG 479
Db 182 TGGTCAAGCTGGGGGTGCTTATCTGCTGGTGGTGGTCAACATGAGCAACCTTGGCTTGG 241
Qy 480 CCGGCGCTCTCTAGTTAGTTAGTGAAGATACCAATTAGAGCCAGAAAGCCCAACAACA 539
Db 242 CCGGCGCTCTCTAGTTAGTTAGTGAAGATACCAATTAGAGCCAGAAAGCCCAACAACA 301
Qy 540 AATACCAATCTCTCAACCAAGAGTGTACTGCTGGCCAGAGGGAGTCCGTAGAGTGC 599
Db 302 AATACCAATCTCTCAACCAAGAGTGTACTGCTGGCCAGAGGGAGTCCGTAGAGTGC 361
Qy 600 GCTGCGCTGTGAAGAGATGCGCGCGTATGATGGAATTAGAGATGGGGTCACTTGGGGC 659
Db 362 GCTGCGCTGTGAAGAGATGCGCGCGTATGATGGAATTAGAGATGGGGTCACTTGGGGC 421
Qy 660 CCAACATTAAGACAGTCTTATTTGGGAGTACTTGCAGATTAAGGGCCCAACTTAAAG 719
Db 422 CCAACATTAAGACAGTCTTATTTGGGAGTACTTGCAGATTAAGGGCCCAACTTAAAG 481
Qy 720 ACTCGGCGCTCTATGCTTGTATCTGCAAGTGAAGACTGTAGAAGTGAATCTTGGTACTTCA 779
Db 482 ACTCGGCGCTCTATGCTTGTATCTGCAAGTGAAGACTGTAGAAGTGAATCTTGGTACTTCA 541
Qy 780 TGGTGAATGTCAAGAGATGCAATCTCATCCGAGATGATGAGAGATGACACCGATGGTCCGG 839
Db 542 TGGTGAATGTCAAGAGATGCAATCTCATCCGAGATGATGAGAGATGACACCGATGGTCCGG 601
Qy 840 AAGATTTTGTCAGTGAGAAAGTAAACAACAAGAGACCACTTGTGACCAACAAGAAA 899
Db 602 AAGATTTTGTCAGTGAGAAAGTAAACAACAAGAGACCACTTGTGACCAACAAGAAA 661
Qy 900 AGATGAGAAAAGCGGCTCATGCTGTGCTGCGGCAACCTGTCAAGTTTGGCTGCCAG 959
Db 662 AGATGAGAAAAGCGGCTCATGCTGTGCTGCGGCAACCTGTCAAGTTTGGCTGCCAG 721
Qy 960 CCGGCGGGGAAACCCAAATGCCAAACCATGCGGTGGCTGAGAAAACGGGAGAGTTTAAAGAG 1019
Db 722 CCGGCGGGGAAACCCAAATGCCAAACCATGCGGTGGCTGAGAAAACGGGAGAGTTTAAAGAG 781
Qy 1020 AGCATGCAATTGAGAGCTCAAGAGTACGAACCAAGCACTGGAGGCTCATTTATGAAAAGTG 1079
Db 782 AGCATGCAATTGAGAGCTCAAGAGTACGAACCAAGCACTGGAGGCTCATTTATGAAAAGTG 841
Qy 1080 TGGTCCCATCTGACAAAGGAAATTAATCTGTGTATGAGAGATGAATACGGGTCCATCA 1139
Db 842 TGGTCCCATCTGACAAAGGAAATTAATCTGTGTATGAGAGATGAATACGGGTCCATCA 901
Qy 1140 ATCAACAGTACCACTGTGATTTGTGAGAGCATGGCTTCAACCGGCCCATCTTCAACCGC 1199
Db 902 ATCAACAGTACCACTGTGATTTGTGAGAGCATGGCTTCAACCGGCCCATCTTCAACCGC 961
Qy 1200 GACTGCGGGCAAAATGCTTCCACAGTGGTCGAGAGAGAGTAGAGTTTGTGCAAGGTTT 1259
Db 962 GACTGCGGGCAAAATGCTTCCACAGTGGTCGAGAGAGAGTAGAGTTTGTGCAAGGTTT 1021
Qy 1260 ACAAGTATGCCCAGACCCCAACATCCAGTGTATCAAGCACTGGGGGATTAATGTTTCA 1319
Db 1022 ACAAGTATGCCCAGACCCCAACATCCAGTGTATCAAGCACTGGGGGATTAATGTTTCA 1081
Qy 1320 ACGGCGCCGAGAGGCTGCCCTTACCTCAAGTGTTCACAGCACTGGGGGATTAATGTTTCA 1379
Db 1082 ACGGCGCCGAGAGGCTGCCCTTACCTCAAGTGTTCACAGCACTGGGGGATTAATGTTTCA 1141
Qy 1380 ATGCAAGAGTGTGGCTGTGT-----TCAATGTGACCGAGCGAGTGTGGGAAATATA 1433
Db 1142 ACAAGAGATTTGAGGTTCTTATATGTGGATGTAACTTTTGAAGAGCTGGGGAAATATA 1201

Qy 1434 TATTAAGTCTTCAATTAATATAGGAGAGCCCAACCAAGTCTGGCTGCTCATGTCCTGCG 1493
Db 1202 CGTCTTGGCGGGATTAATTTCTATTTGGATATCTTTTCACTGTGATGTTGACAGTTCTGCG 1261
Qy 1494 CAAGACAGAAAGCGCTGGAAGGAAAGAGATTAACGTTTCCCAAGTACTTGGAGCA 1553
Db 1262 C-----AGGCGCTGGAAGGAAAGAGATTAACGTTTCCCAAGTACTTGGAGCA 1312
Qy 1554 TACCATTTATCTGCAATAGGGGTCTTCTTAATGCGCTGATATGAGTGAACGATCCTGT 1613
Db 1313 TACCATTTATCTGCAATAGGGGTCTTCTTAATGCGCTGATATGAGTGAACGATCCTGT 1372
Qy 1614 GCCGAATGAAGAACAGCAACCAAGAGCCAGACTTTCAGACAGCCAGCGGCTGTGCAAGC 1673
Db 1373 GCCGAATGAAGAACAGCAACCAAGAGCCAGACTTTCAGACAGCCAGCGGCTGTGCAAGC 1432
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Db 1493 TGAATCTCAACACCCGCTGTGTGAGATTAACAACGCTCTCTTCAACGCGAGACACC 1552
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Qy 1854 GAGATTAAGTGAACACTGTGGCAAGCCCTGCGGAGAGTTCCTTGGCAAGTGTCAATGG 1913
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Qy 2034 TGAAGATGATTTGGGAAACACAAAGATATCAATAATCTTCTTGAAGCTGTGACACAGATG 2093
Db 1793 TGAAGATGATTTGGGAAACACAAAGATATCAATAATCTTCTTGAAGCTGTGACACAGATG 1852
Qy 2094 GGCCTCTTATGTCTATGTTGATGATGCTCTTAAGGCAACCTTCCAGAAATACCTCCGAG 2153
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Qy 2214 TGAACCTTCAAGGACTTGTGTCAATGCACTTACAGAGTGGCCAGACGAGTGAATCTTGG 2273
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Qy 2274 CTTCCCAAAAATGATTCATGAGATTTAGACGACCAAGAAATGTTTGGTAAACGAAAACA 2333
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QY 2514 CTTTAAAGGGGCTGCGCCCTTACCAAGGATTCGGTGAAGAACTTTTAAAGCTGCTGAAG 2573
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 DB 2333 AAGGACAGAGATGATTAAGCAAGGCACTGACCAAGCAATGTCATGATGATGAGG 2392
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 DB 2393 ACTGTTGCGATGAGTGCCTCCCAAGACCAAGCTTCAAGAGCTTGTAGAAGACTTG 2452
 QY 2694 ATCGAATTCCTCACTCTCAACAACCAATGAGGAATCTTGAAGCTCAGCCAACTCTGAAC 2753
 DB 2453 ATCGAATTCCTCACTCTCAACAACCAATGAGGAATCTTGAAGCTCAGCCAACTCTGAAC 2512
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 DB 2693 GGTACACTGAGCAGGAGACCATGCTCCCAAGAGCTTGTGCTGCTGCTGCTGCTGCTG 2752
 QY 2994 ATCAGAGAGTAATAATGTAAGAAATGATCAGCATATGTAAGATTTAATACAGTTGA 3053
 DB 2753 ATCAGAGAGTAATAATGTAAGAAATGATCAGCATATGTAAGATTTAATACAGTTGA 2812
 QY 3054 AAACCTGTATCTTCCCGAGAGAGAAAGGTTCTGAGAGAGTGGACTGC 3106
 DB 2813 AAACCTGTATCTTCCCGAGAGAGAAAGGTTCTGAGAGAGTGGACTGC 2865

RESULT 8
 US-08-323-430-15
 ; Sequence 15, Application US/08323430
 ; Patent No. 6344546
 ; GENERAL INFORMATION:
 ; APPLICANT: Dione, Craig A
 ; APPLICANT: Crumley, Greg
 ; APPLICANT: Schlessinger, Joseph
 ; TITLE OF INVENTION: Fibroblast Growth Factor Receptors
 ; NUMBER OF SEQUENCES: 15
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Rhone-Poulenc Rorer Legal Department
 ; STREET: 500 Arcola Road
 ; CITY: Collegeville
 ; STATE: PA
 ; COUNTRY: USA
 ; ZIP: 19426
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/323,430
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US to be assigned
 ; FILING DATE: 21-AUG-1992
 ; APPLICATION NUMBER: US 07/549,587
 ; FILING DATE: 06-JUL-1990

; ATTORNEY/AGENT INFORMATION:
 ; NAME: Goodman, Rosanne
 ; REGISTRATION NUMBER: 32,534
 ; REFERENCE/DOCKET NUMBER: A0496
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (215) 454-3817
 ; TELEFAX: (215) 454-3808
 ; INFORMATION FOR SEQ ID NO: 15:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 3416 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA
 ; US-08-323-430-15

Query Match 87.4%; Score 2714.2; DB 3; Length 3416;
 Best Local Similarity 97.1%; Pred. No. 0;
 Matches 2790; Conservative 0; Mismatches 68; Indels 15; Gaps 2;

QY 240 CACAGGTGCGGAGAGAGGCTTCCATTCAAGTGAATGACAGAGCAGCCAGCGCTCGGT 299
 DB 2 CACAGGTGCGGAGAGAGGCTTCCATTCAAGTGAATGACAGAGCAGCCAGCGCTCGGT 61
 QY 300 TCCAGGCGCCAGCGAGCTGAAGGCAATGCGGTAGTCCATGCTCCGTAGAGAACTGTGC 359
 DB 62 TCCAGGCGCCAGCGAGCTGAAGGCAATGCGGTAGTCCATGCTCCGTAGAGAACTGTGC 121
 QY 360 AGATGGATTTAAGTCCACATGAGATATGGAAGAGACCGGGAGTTGGTACCTTAACCA 419
 DB 122 AGATGGATTTAAGTCCACATGAGATATGGAAGAGACCGGGAGTTGGTACCTTAACCA 181
 QY 420 TGGTCAAGTGGGGGTGTTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 479
 DB 182 TGGTCAAGTGGGGGTGTTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 241
 QY 480 CCGGCGCTCTCTTCAAGTTAGTGAATGCCATTTAGAGCCAGAGAGCCAGCAACCA 539
 DB 242 CCGGCGCTCTCTTCAAGTTAGTGAATGCCATTTAGAGCCAGAGAGCCAGCAACCA 301
 QY 540 AATACCAATCTCTCAACCAAGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 599
 DB 302 AATACCAATCTCTCAACCAAGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 361
 QY 600 GCTGCTGTTGAAAGATGCGCGCGCTGATGATGATGATGATGATGATGATGATGATGATG 659
 DB 362 GCTGCTGTTGAAAGATGCGCGCGCTGATGATGATGATGATGATGATGATGATGATGATG 421
 QY 660 CCAACAAATAGACAGTGTATTTGGGAGTACTTGCAGATTAAGGCGCCACACTAGAG 719
 DB 422 CCAACAAATAGACAGTGTATTTGGGAGTACTTGCAGATTAAGGCGCCACACTAGAG 481
 QY 720 ACTCGGCTCTATGCTTGTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 779
 DB 482 ACTCGGCTCTATGCTTGTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 541
 QY 780 TGGTGAATGTCAAGATGTCATCTCATCCGAGATGATGATGATGATGATGATGATGATGATG 839
 DB 542 TGGTGAATGTCAAGATGTCATCTCATCCGAGATGATGATGATGATGATGATGATGATGATG 601
 QY 840 AAGATTTTGTAGTGAAGACAGTAAACAAAGAGAGCACTATGAGCAACACAGAA 899
 DB 602 AAGATTTTGTAGTGAAGACAGTAAACAAAGAGAGCACTATGAGCAACACAGAA 661
 QY 900 AGATGAAAAGCGGCTCCATGCTGTGCTGCGGCAACCTGTCAAGTTTCCGTGCGCAG 959
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 QY 960 CCGGGGGGAAACCAATGCCAACCAATGCCGTGCTGAAAACCGGGAGAGTTAAGCAG 1019
 DB 722 CCGGGGGGAAACCAATGCCAACCAATGCCGTGCTGAAAACCGGGAGAGTTAAGCAG 781
 QY 1020 AGCATGCATTTGAGGCTACAAAGTACGAAACCAAGCACTGAGCTCATTTATGAAAGTG 1079

DB 782 AGCATGCAATTTGGAGGCTTACAGAGTACGAAACCGACTGAGCTCATTTATGAAAGTGC 841
QY 1080 TGGTCCCATCTGACAAAGGAAATTTATACCTGTGTAGTGAAGATGAATACGGGTCCATCA 1139
DB 842 TGGTCCCATCTGACAAAGGAAATTTATACCTGTGTGTGAGAAATGAATACGGGTCCATCA 901
QY 1140 ATCAACAGTACACACTGTGATTTGTGAGAGGATGTGCTTCAACGGGCCATCTCCAGACCG 1199
DB 902 ATCAACAGTACACACTGTGATTTGTGAGAGGATGTGCTTCAACGGGCCATCTCCAGACCG 961
QY 1200 GACTGCGGCAAAATGCTCCCAAGTGTGCGGAGGAGAGTGAAGTTTGTCTGCAAGGTTT 1259
DB 962 GACTGCGGCAAAATGCTCCCAAGTGTGCGGAGGAGAGTGAAGTTTGTCTGCAAGGTTT 1021
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DB 1082 ACCGGCCCCGAGCGGCTGCTTCACTCAAGGTTCTCAAGGCGCGCGGTGTTAACACACGCG 1141
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DB 1142 ACAAGAGATTTGAGGTTCTCTATATTGGAAATGTAACTTTTGAAGACGCTGCGGGAATATA 1201
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QY 1494 CAAGAACGCAAGCCCTGTGAAAGAAAGAGATTAAGGTTTCCCGACATCACTGTGAGA 1553
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QY 1554 TAGCCATTTACTGTGATTTGGGGTCTTCTTAATGCGCTGTATGTGTTAAAGTCACTGCTGT 1613
DB 1313 TAGCCATTTACTGTGATTTGGGGTCTTCTTAATGCGCTGTATGTGTTAAAGTCACTGCTGT 1372
QY 1614 GCCCAATGAAGAACACGACCAAGAGGCGACATTCAGACAGCGCGGCTGTGACAGC 1673
DB 1373 GCCCAATGAAGAACACGACCAAGAGGCGACATTCAGACAGCGCGGCTGTGACAGC 1432
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DB 1433 TGACCAAAAGTATCCCTCTGTGAGAGAGAGTTAAAGTTTGGCTGAGTCCAGCTCTTCA 1492
QY 1734 TGAATCTCAACACCCCGCTGTGTGAGATTAACAACGCTCTCTTCAACGCGACAGACCC 1793
DB 1493 TGAATCTCAACACCCCGCTGTGTGAGATTAACAACGCTCTCTTCAACGCGACAGACCC 1552
QY 1794 CCATGCTGTGAGAGGGGTCTCCAGATATGAACTTCCAGAGAACCCAAATTTGGAGTTTCCAA 1853
DB 1553 CCATGCTGTGAGAGGGGTCTCCAGATATGAACTTCCAGAGAACCCAAATTTGGAGTTTCCAA 1612
QY 1854 GAGATTAAGCTGACACTGTGCGCAAGCCCTGTGAGAGAGGTTGCTTTGGCGAAGTGTCAATGG 1913
DB 1613 GAGATTAAGCTGACACTGTGCGCAAGCCCTGTGAGAGAGGTTGCTTTGGCGAAGTGTCAATGG 1672
QY 1914 CGGAAGAGTGTGGAAATTTGACAAAGACAAAGCCCAAGAGAGCGGTCAACGCTGTGAGAGA 1973
DB 1673 CGGAAGAGTGTGGAAATTTGACAAAGACAAAGCCCAAGAGAGCGGTCAACGCTGTGAGAGA 1732
QY 1974 TGTGAAAGATGATGTCACAGAGAAAGACTTTTCTGTATCTGTGTCTGAGAGATGAGATGA 2033
DB 1733 TGTGAAAGATGATGTCACAGAGAAAGACTTTTCTGTATCTGTGTCTGAGAGATGAGATGA 1792
QY 2034 TGAAGATGATTTGGGAAACAAAGATATCATTAATCTTTCTGTGAGCTGTGACACAGATG 2093
DB 1793 TGAAGATGATTTGGGAAACAAAGATATCATTAATCTTTCTGTGAGCTGTGACACAGATG 1852
QY 2094 GGCTCTCTATGTATGTTGATGTGCTTAAAGGCAACTCCGGAATACCTCCGAG 2153

DB 1853 GGCTCTCTATGTATGATTTGAGTATGCTTAAAGCAACTCCGAGATATCTCCGAG 1912
QY 2154 CCGGAGGCGACCCCGGAGTGAAGTACTCTCATTAAGCATTAACGCTGTCTGAGAGACAGA 2213
DB 1913 CCGGAGGCGACCCCGGAGTGAAGTACTCTCATTAAGCATTAACGCTGTCTGAGAGACAGA 1972
QY 2214 TGACCTTCAAGAGCTTGTGTGACCTTACAGAGTGTGCTTCAAGAGTGTGCTTCAAGAGTGTG 2273
DB 1973 TGACCTTCAAGAGCTTGTGTGACCTTACAGAGTGTGCTTCAAGAGTGTGCTTCAAGAGTGTG 2032
QY 2274 CTTCGCAAAATATGATTCATGAGATTTAGACACCGAATTTGTTGTGTAAGAAACA 2333
DB 2033 CTTCGCAAAATATGATTCATGAGATTTAGACACCGAATTTGTTGTGTAAGAAACA 2092
QY 2334 ATGTGATGAATAATGACAGCTTTGAGACTGGCCGAGATATCAACATTAATGATTAATCA 2393
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QY 2394 AAAAGACCAATTTGGGCGGCTTCCAGTCAAGTGTGCTTCCAGAAAGCCCTGTTGATA 2453
DB 2153 AAAAGACCAATTTGGGCGGCTTCCAGTCAAGTGTGCTTCCAGAAAGCCCTGTTGATA 2212
QY 2454 GAGTATACACTCATGAGATGATGTGTGCTTGTGGGGTGTAAATGTGAGATCTTCA 2513
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QY 2514 CTTTAAAGGGGCTGCGCTTACCCAGGAAATTTCCGTGAGAGAACTTTTAACTGTCTGAAG 2573
DB 2273 CTTTAAAGGGGCTGCGCTTACCCAGGAAATTTCCGTGAGAGAACTTTTAACTGTCTGAAG 2332
QY 2574 AAGGACACAGATGATTAAGCCAGCCAACTGACCAAGAACTGTACATGATGATGAGG 2633
DB 2333 AAGGACACAGATGATTAAGCCAGCCAACTGACCAAGAACTGTACATGATGATGAGG 2392
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DB 2393 ACTGTGTGACATGAGTGTGCTTCCAGAGCAAGCTTCAAGAGTGTGTAAGAACTTGG 2452
QY 2694 ATGGAATTTCACTTCTCAACCAATGAGAAATTTGAACTTCAAGCTTCAAGCTTCAAGC 2753
DB 2453 ATGGAATTTCACTTCTCAACCAATGAGAAATTTGAACTTCAAGCTTCAAGCTTCAAGC 2512
QY 2754 AGTATTCACCTAGTTACCCCTGACACAAAGAACTTGTCTTCAAGAGATGATTTGTT 2813
DB 2513 AGTATTCACCTAGTTACCCCTGACACAAAGAACTTGTCTTCAAGAGATGATTTGTT 2572
QY 2814 TTTCTCAGAGCCCATGCTTACGAACCAATGCTTCTCAGATTCACACATTAACGGCA 2873
DB 2573 TTTCTCAGAGCCCATGCTTACGAACCAATGCTTCTCAGATTCACACATTAACGGCA 2632
QY 2874 GTGTTAAACATGAATGACTGTGTGTGCTGTGCTTCCCAACAGACAGCACTGGGAACCTTA 2933
DB 2633 GTGTTAAACATGAATGACTGTGTGTGCTGTGCTTCCCAACAGACAGCACTGGGAACCTTA 2692
QY 2934 GCTTACCTGAGGAGGAGACATGCTTCCAGAGCTTGTGTCTTCACTGTGATTAATGG 2993
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DB 2753 ATCAGAGAGTAAATATTTGAAAGATATCAGCATATGTGTAAAGATTTATACAGTTGA 2812
QY 3054 AAACTGTATCTTTCCCGAGAGAGAAAGGTTTCTGAGACAGTGTGACTGC 3106
DB 2813 AAACTGTATCTTTCCCGAGAGAGAAAGGTTTCTGAGACAGTGTGACTGC 2865

RESULT 9
US-09-954-556-24
; Sequence 24, Application US/09954556
; Patent No. 6900053
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia

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APPLICANT: Susan M. Freier
APPLICANT: Scott Cooper
TITLE OF INVENTION: ANTISENSE MODULATION OF FIBROBLAST GROWTH FACTOR RECEPTOR 2 EXPRE
FILE REFERENCE: R15-0250
CURRENT APPLICATION NUMBER: US/09/954,556
CURRENT FILING DATE: 2001-09-14
NUMBER OF SEQ ID NOS: 108
SEQ ID NO 24
LENGTH: 3244
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (488) ... (2605)
US-09-954-556-24

Query Match      74.9%; Score 2327.4; DB 3; Length 3244;
Best Local Similarity 88.3%; Pred. No. 0;
Matches 2749; Conservative 0; Mismatches 6; Indels 358; Gaps 6;

QY 1 CCCGCGAGCAAAAGTTGTGTGAGCAACG-CAAGCTGAGTCTTTCTTCTGTTCC 59
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QY 60 CCAATTCGAGGCGAGCCGCGGCGTCTATG--GGCTTCTCCGAGGCTGGGTTACCG 116
DB 123 CCAATTCGAGGCGAGCCGCGGCGTCTATGCGCGGCTCTCCGAGGCTGGGTTACCG 182
QY 117 GTGAACCCGCGGAGGCTGGCGCGGGAAGAACCAAGACCACTCTTCTGCTTTGAG 176
DB 183 GTGAACCCGCGGAGGCTGGCGCGGGAAGAACCAAGACCACTCTTCTGCTTTGAG 242
QY 177 TTGCTCCCGCAACCCCGGCGTGTGCTTCTCATCCGACCAACGCGGCGC-CGGG 235
DB 243 TTGCTCCCGCAACCCCGGCGTGTGCTTCTCATCCGACCAACGCGGCGC-CGGG 302
QY 236 ACAACACAGGTCCGCGAGAGGCTTGCATTCAAGTGACTGACGACGAC-CCAGCGCC 294
DB 303 ACAACACAGGTCCGCGAGAGGCTTGCATTCAAGTGACTGACGACGACGACGCGC 362
QY 295 TCGGTTCTGAGGCCACCGCA-CTGTAAGGCAATTGCGGTAATCCCTGAGAGAA 353
DB 363 TCGGTTCTGAGGCCACCGGAGGCTGAAGGCAATTGCGGTAATCCCTGAGAGAA 422
QY 354 GTGTGAGATGGAGTTAACTCCATGAGATATGAGAGAGAACCGGGAGTTGTACCG 413
DB 423 GTGTGAGATGGAGTTAACTCCATGAGATATGAGAGAGAACCGGGAGTTGTACCG 482
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DB 483 TAAACATGTCACTGGGGTCTTTTCACTGCTGTGTGTCAACATGAGCAACTTGT 542
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DB 723 TGGGGCCCAACATATGAGAGAGTGTATTTGGGGAGTCTTGAGATTAAGGCGCCAC 782
QY 714 CTAGAGACTCGGCTCTATGCTTTGATCTGCACTAGAGACTGTAGACAGTGAACCTTGAT 773
DB 783 CTAGAGACTCGGCTCTATGCTTTGATCTGCACTAGAGACTGTAGACAGTGAACCTTGAT 842
QY 774 ACTTCATGTGATGTCAAGATGCCATCTCATCCGAGATGATGAGATGACCCGATG 833
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DB 843 ACTTCATGTGATGTCAAGATGCCATCTCATCCGAGATGATGAGATGACCCGATG 902
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DB 903 GTGCGAAAGTTTGTCTAGTGAAGACAGTAAACAAAGAGACACATCTGACCAACA 962
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DB 963 CAGAAAGATGAAAGGGGCTCCATGCTGTGCGCGGCGCAACATCTCAAGTTTGCT 1022
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DB 1023 GCCCAGCCGGGGGAAACCAATGCCCAATGCGGTGCTGAAAAACGGGAAGATTGA 1082
QY 1014 AGCAGAGCATGCACTTGAAGGCTTCAAGGTACAAACAGACACCTGAGGCTCATTAAG 1073
DB 1083 AGCAGAGCATGCACTTGAAGGCTTCAAGGTACAAACAGACACCTGAGGCTCATTAAG 1142
QY 1074 AAAGTGTGTCATCTGACAAAGGAAATTAATCTGTGTGTGAGATGAATACGGGT 1133
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DB 1263 AAGCGGACTCGCGCAATGCTTCAACAGTGTGTGAGAGAGAGTGAAGTTGTCTGCA 1322
QY 1254 AGGTTTACAGTATGCCAGAGCCCAATCCAGTGTATCAAGCACTGTGAAAAAGACGA 1313
DB 1323 AGGTTTACAGTATGCCAGAGCCCAATCCAGTGTATCAAGCACTGTGAAAAAGACGA 1382
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DB 1383 GTAAATACCGGCGCGCAAGGCGCTGCCCTTCAAGGTTCTCAAG----- 1426
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DB 1427 ----- 1426
QY 1434 TATGTAAAGTCTCAATTAATATAGGAGAGCCCAACAGTCTGCTCACTGTCTGCG 1493
DB 1427 ----- 1426
QY 1494 CAAAACAGCAGCGCTGGAAGAGAAAAAGAGATTACAGCTTCCCAAGCTACCTGGAGA 1553
DB 1427 ----- 1426
QY 1554 TAGCAATTTACTGATAGGGGCTTCTTAATGCGCTGTATGTGTGAACAGTCACTGT 1613
DB 1427 ----- 1426
QY 1614 GCGGATGAAGAAACAGACCAAGAAAGCAGATTGACAGACCGCGCTGTGACAAAGC 1673
DB 1427 ----- 1426
QY 1674 TGACCAACGTATCCCTCTGCGAGACAGGTAAAGTTTCGGCTGAGTCAAGTCTCTCA 1733
DB 1427 ----- 1426
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QY 1794 CCAATGCTGCAAGGGCTCCGAGTATGAACCTTCCAGAGAACCAAAATGGAGTTTCCA 1853
DB 1512 CCAATGCTGCAAGGGCTCCGAGTATGAACCTTCCAGAGAACCAAAATGGAGTTTCCA 1571
QY 1854 GAGATTAAGCTGACACTGGGCAAGCCCTGTGGAAGAGTTTCTTTGGGCAAGTGTCTATGG 1913
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Db 1572 GAGATTAAGCTGACCTGGGCAAGCCCTGGGAGAAAGTTGCTTTGGGCAAGTGTCTATGG 1631
Qy 1914 CGAAGCACTGGGAATTTGACAAAGACAAAGCCCAAGAGGCGGTACCGTGGCCGTGAAGA 1973
Db 1632 CGAAGCACTGGGAATTTGACAAAGACAAAGCCCAAGAGGCGGTACCGTGGCCGTGAAGA 1691
Qy 1974 TGTGAAAGATGATGACCAAGAAAGACCTTTCTGATCTGGTCTCAGAGATGAGATGA 2033
Db 1692 TGTGAAAGATGATGACCAAGAAAGACCTTTCTGATCTGGTCTCAGAGATGAGATGA 1751
Qy 2034 TGAAGATGATTTGGGAAACAAAGAAATATCATAAATCTTCTTGGAGCCCTGACACAGATG 2093
Db 1752 TGAAGATGATTTGGGAAACAAAGAAATATCATAAATCTTCTTGGAGCCCTGACACAGATG 1811
Qy 2094 GGGCTCTTATGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2153
Db 1812 GGGCTCTTATGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1871
Qy 2154 CCGGAGAGCCCAACCGGAGATGAGATGATGATGATGATGATGATGATGATGATGATGATG 2213
Db 1872 CCGGAGAGCCCAACCGGAGATGAGATGATGATGATGATGATGATGATGATGATGATGATG 1931
Qy 2214 TGACCTTCAAGGACTTGGTGTCTATGCACTACAGCTGGCCAGACGAGATGAGTACTTGG 2273
Db 1932 TGACCTTCAAGGACTTGGTGTCTATGCACTACAGCTGGCCAGAGGCAATGAGTACTTGG 1991
Qy 2274 CTTCCCAAAAATGATATTCATGAGATTTTGAAGCCAGAAATGTTTGGTAAACAGAAAA 2333
Db 1992 CTTCCCAAAAATGATATTCATGAGATTTTGAAGCCAGAAATGTTTGGTAAACAGAAAA 2051
Qy 2334 ATGTGATGAAATATGACAGACTTTGACCTGCGCAGAGATATCAAAATATTAATTAATTA 2393
Db 2052 ATGTGATGAAATATGACAGACTTTGACCTGCGCAGAGATATCAAAATATTAATTAATTA 2111
Qy 2394 AAAAGACCAAAATGGGCGGCTCCAGTCAAGTGGATGGCTCCAGAAACCTGTTTGATA 2453
Db 2112 AAAAGACCAAAATGGGCGGCTCCAGTCAAGTGGATGGCTCCAGAAACCTGTTTGATA 2171
Qy 2454 GAGATATCACTCATCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2513
Db 2172 GAGATATCACTCATCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2231
Qy 2514 CTTTAAAGGGGCTGCGCCCTTACCAAGAGATTTCCCTGGAGAGAACTTTTAAAGCTGCGAAG 2573
Db 2232 CTTTAAAGGGGCTGCGCCCTTACCAAGAGATTTCCCTGGAGAGAACTTTTAAAGCTGCGAAG 2291
Qy 2574 AAGGACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2633
Db 2292 AAGGACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2351
Qy 2634 ACTGTTGCAATGCAAGTGGCTTCCAGAGACCAACGTTTCAAGCAATGTTGTAAGAACTTGG 2693
Db 2352 ACTGTTGCAATGCAAGTGGCTTCCAGAGACCAACGTTTCAAGCAATGTTGTAAGAACTTGG 2411
Qy 2694 ATCGAATTTCTCATCTTCAACCAATGAGAAATATTTGAGACTTCAAGCCAACTTCCGAC 2753
Db 2412 ATCGAATTTCTCATCTTCAACCAATGAGAAATATTTGAGACTTCAAGCCAACTTCCGAC 2471
Qy 2754 AGATATTCACCTAGTAACTCTGACCAAGAAAGTTCTTGTCTTCAAGAGATGATGATGATG 2813
Db 2472 AGATATTCACCTAGTAACTCTGACCAAGAAAGTTCTTGTCTTCAAGAGATGATGATGATG 2531
Qy 2814 TTTCTCCAGACCCCAATGCTTACGAACCAATGCTTCTCAAGTATCACAACATTAACGCGCA 2873
Db 2532 TTTCTCCAGACCCCAATGCTTACGAACCAATGCTTCTCAAGTATCACAACATTAACGCGCA 2591
Qy 2874 GTGTTAAACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2933
Db 2592 GTGTTAAACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2651
Qy 2934 GCTACACTGAGAGAGAGACATGCTCCAGAGGCTTGTGTCTCACTTGTATATATG 2993
Db 2652 GCTACACTGAGAGAGAGACATGCTCCAGAGGCTTGTGTCTCACTTGTATATATG 2711

Qy 2994 ATCAGAGAGATTAATATTTGAAAGATATCAGATATGTATAAGATTTATACAGTTGA 3053
Db 2712 ATCAGAGAGATTAATATTTGAAAGATATCAGATATGTATAAGATTTATACAGTTGA 2771
Qy 3054 AAACCTTGAATCTTCCCAAGAGAGAGAAAGGTTTCTGAGCAGTGAAGTGC 3106
Db 2772 AAACCTTGAATCTTCCCAAGAGAGAGAAAGGTTTCTGAGCAGTGAAGTGC 2824

RESULT 10
US-09-954-556-28
; Sequence 28, Application US/09954556
; Patent No. 6900053
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freiler
; TITLE OF INVENTION: ANTISENSE MODULATION OF FIBROBLAST GROWTH FACTOR RECEPTOR 2 EXP
; FILE REFERENCE: RTS-0250
; CURRENT APPLICATION NUMBER: US/09/954,556
; NUMBER OF SEQ ID NOS: 108
; SEQ ID NO 28
; LENGTH: 2650
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-954-556-28

Query Match 74.7%; Score 2320; DB 3; Length 2650;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 2323; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 395 GGAACCGGAGATGTTGATACCGTACATGCTGAGCTGGGGTGTTCATCTGCTGTGTGTG 454
Db 1 GGAACCGGAGATGTTGATACCGTACATGCTGAGCTGGGGTGTTCATCTGCTGTGTGTG 60
Qy 455 GTCAACATGCGCAACCTTGTCCCTGCGCCGCTCTTCAAGTTAGTTAGAGATACACA 514
Db 61 GTCAACATGCGCAACCTTGTCCCTGCGCCGCTCTTCAAGTTAGTTAGAGATACACA 120
Qy 515 TTAGAGCAGAGAGACCAACCAATATCAATCTCTCAACCAAGATGATGATGATGATG 574
Db 121 TTAGAGCAGAGAGACCAACCAATATCAATCTCTCAACCAAGATGATGATGATGATG 180
Qy 575 GCGCCAGGGAGTGTGCTAGAGTGTGCTGCTGTTTGAAGATGCGCCGTGATCAATGG 634
Db 181 GCGCCAGGGAGTGTGCTAGAGTGTGCTGCTGTTTGAAGATGCGCCGTGATCAATGG 240
Qy 635 ACTAAGATGAGGGTGTGCTGAGAGTGTGCTGCTGTTTGAAGATGCGCCGTGATCAATGG 694
Db 241 ACTAAGATGAGGGTGTGCTGAGAGTGTGCTGCTGTTTGAAGATGCGCCGTGATCAATGG 300
Qy 695 CAGATTAAGGGCGCCACACTAGAGACTCCGGCTCTATGCTTGAAGTGAAGTGAAGTGA 754
Db 301 CAGATTAAGGGCGCCACACTAGAGACTCCGGCTCTATGCTTGAAGTGAAGTGAAGTGA 360
Qy 755 GTAGACAGTGAACCTTGTGATCTTCAATGATGATGATGATGATGATGATGATGATGATG 814
Db 361 GTAGACAGTGAACCTTGTGATCTTCAATGATGATGATGATGATGATGATGATGATGATG 420
Qy 815 GATGAGATGACACCGATGAGTGTGCGGAGATTTTGTGAGTGAAGACAGTGAACAGAGA 874
Db 421 GATGAGATGACACCGATGAGTGTGCGGAGATTTTGTGAGTGAAGACAGTGAACAGAGA 480
Qy 875 GCACCATATCTGACCAACAGAAAGATGAGAAAGGCTCTCAATGCTGTGCTGCGGCC 934
Db 481 GCACCATATCTGACCAACAGAAAGATGAGAAAGGCTCTCAATGCTGTGCTGCGGCC 540
Qy 935 AAACCTGCAAGTTTGTGCTGCTGCGCCAGCGGGGGGAAACCAATGCAACATGCGGTGTG 994
Db 541 AAACCTGCAAGTTTGTGCTGCTGCGCCAGCGGGGGGAAACCAATGCAACATGCGGTGTG 600

QY 995 AAAAAAGGAGAGATTAAAGCAGAGACATCGCATTTGGAGGCTTACAAAGTACGAAACCG 1054
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 QY 1055 CACTGGAGGCTCATTTAGAAAAGTGTGTCCCATCTGACAAAGGGAATTTATCTGTGTA 1114
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 QY 1115 GTGAGAGATGAATACGGGTCATCATCAACGTAACACTGGAATGTTGTGAGCGATCG 1174
 Db 721 GTGAGAGATGAATACGGGTCATCATCAACGTAACACTGGAATGTTGTGAGCGATCG 780
 QY 1175 CTTCAACGGGCCATCTCTCAAGCCGGAATGCGGCAAAATGCTTCAAGTGTGCGAGGA 1234
 Db 781 CTTCAACGGGCCATCTCTCAAGCCGGAATGCGGCAAAATGCTTCAAGTGTGCGAGGA 840
 QY 1235 GAGGTAGATTGTTCTGCAAGGTTTACATGTAATGCCAGCCCAATCCATCCAGTGAATCA 1294
 Db 841 GAGGTAGATTGTTCTGCAAGGTTTACATGTAATGCCAGCCCAATCCATCCAGTGAATCA 900
 QY 1295 CAGGTGAGAAAAGAACGAGTAATACGGGCGCGAGCGGCTGCTTACCTCAAGGTTCTC 1354
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 QY 1355 AAGCACTCGGGGATTAATAGTTCCATGAGGAAGTGTGCTGCTTCAATGTGACCGAG 1414
 Db 961 AAGCACTCGGGGATTAATAGTTCCATGAGGAAGTGTGCTGCTTCAATGTGACCGAG 1020
 QY 1415 GCGGATCTGGGGAATTAATATGTAAGTCTCCAAATTAATAGGAGGCAACAGTCT 1474
 Db 1021 GCGGATCTGGGGAATTAATATGTAAGTCTCCAAATTAATAGGAGGCAACAGTCT 1080
 QY 1475 GCGTGTCTCATGTTCTGCGCAAAACAGCAAGCGCTTGAGAGAAAAGAGATTACGCT 1534
 Db 1081 GCGTGTCTCATGTTCTGCGCAAAACAGCAAGCGCTTGAGAGAAAAGAGATTACGCT 1140
 QY 1535 TCCCAAGACTAACCTGAGATGATGCAATTAATGAGGGGCTTCTTAATGCGCTGATG 1594
 Db 1141 TCCCAAGACTAACCTGAGATGATGCAATTAATGAGGGGCTTCTTAATGCGCTGATG 1200
 QY 1595 GTGGTAACAGTCACTCTGTGCGAATGAGAAACAGAACCAAGAACCAAGTTCAGAGAC 1654
 Db 1201 GTGGTAACAGTCACTCTGTGCGAATGAGAAACAGAACCAAGAACCAAGTTCAGAGAC 1260
 QY 1655 CAGCGGCTGTGCAAAAGCTGACCAAACTATCCCTCGGAGAGACAGTTACGTTTCG 1714
 Db 1261 CAGCGGCTGTGCAAAAGCTGACCAAACTATCCCTCGGAGAGACAGTTACGTTTCG 1320
 QY 1715 GCTGAGTCCAGCTCTCATGTAATCTCAACACCCCGTGTGAGGATTAACACAGGCTC 1774
 Db 1321 GCTGAGTCCAGCTCTCATGTAATCTCAACACCCCGTGTGAGGATTAACACAGGCTC 1380
 QY 1775 TCTTCAACGAGCAACCCCATCTGAGCAAGGGTCTTCCGATGTAATCTTCCAGAGAC 1834
 Db 1381 TCTTCAACGAGCAACCCCATCTGAGCAAGGGTCTTCCGATGTAATCTTCCAGAGAC 1440
 QY 1835 CCAAAATGGAGTTTCCAAAGATTAAGCTGCACTGGGCAAGCCCTGGGGAAGGTTGC 1894
 Db 1441 CCAAAATGGAGTTTCCAAAGATTAAGCTGCACTGGGCAAGCCCTGGGGAAGGTTGC 1500
 QY 1895 TTTGGGCAAGTGTGATGCGGAGAGAGAGTGGAAATTGACAAAGCAAGCCCAAGAGCG 1954
 Db 1501 TTTGGGCAAGTGTGATGCGGAGAGAGAGTGGAAATTGACAAAGCAAGCCCAAGAGCG 1560
 QY 1955 GTCAACCGTGGCCGTGAAGATTTGAAGATGATGCAACAGAGAAAGCTTTTGATCTG 2014
 Db 1561 GTCAACCGTGGCCGTGAAGATTTGAAGATGATGCAACAGAGAAAGCTTTTGATCTG 1620
 QY 2015 GTGTCAAGATGAGATGATGAAGTGAATTTGGGAAAACAAAGATATATATAATCTTCTT 2074
 Db 1621 GTGTCAAGATGAGATGATGAAGTGAATTTGGGAAAACAAAGATATATATAATCTTCTT 1680
 QY 2075 GGAACCTGTCAACAGGATGGGCTCTCTATGTCAATGTTGAGTATGCTTAAAGGCAAC 2134

Db 1681 GGAACCTGTCAACAGGATGGGCTCTCTATGTCAATGTTGAGTATGCTTAAAGCAAC 1740
 QY 2135 CTCGAGAAATACCTCCGAGCCCGGAGCCACCCGGAGTGAATCTCTATGACATTAAAC 2194
 Db 1741 CTCGAGAAATACCTCCGAGCCCGGAGCCACCCGGAGTGAATCTCTATGACATTAAAC 1800
 QY 2195 CGTGTCTCGAGAGAGATGACCTTCAAGGACTTGTGTCAATGACCTACAGGCTGGCC 2254
 Db 1801 CGTGTCTCGAGAGAGATGACCTTCAAGGACTTGTGTCAATGACCTACAGGCTGGCC 1860
 QY 2255 AGAGGATGGAATCTTGGCTTCCCAAAATGTAATCATCGAATTTAGCAAGCCAGAAAT 2314
 Db 1861 AGAGGATGGAATCTTGGCTTCCCAAAATGTAATCATCGAATTTAGCAAGCCAGAAAT 1920
 QY 2315 GTTTTGTAAACAGAAAACAAATGATGAATAATGCACTTTGAGCTCCGACAGATATC 2374
 Db 1921 GTTTTGTAAACAGAAAACAAATGATGAATAATGCACTTTGAGCTCCGACAGATATC 1980
 QY 2375 AACATATGACTATTAACAAAAGACCAACATGGGCGCTTCCAGTCAAGTGAATGGCT 2434
 Db 1981 AACATATGACTATTAACAAAAGACCAACATGGGCGCTTCCAGTCAAGTGAATGGCT 2040
 QY 2435 CCAGAGCCCTGTTGTAGATGATTAACACTCATCAAGTGAATGTCTGCTTCCGAGTG 2494
 Db 2041 CCAGAGCCCTGTTGTAGATGATTAACACTCATCAAGTGAATGTCTGCTTCCGAGTG 2100
 QY 2495 TTAATGTGAGATCTTCACTTTAGGGGCTCGCCTTACCCAGGATTTCCCTGGAGGA 2554
 Db 2101 TTAATGTGAGATCTTCACTTTAGGGGCTCGCCTTACCCAGGATTTCCCTGGAGGA 2160
 QY 2555 CTTTAAAGCTGTGAAGAGAGACAGAAATGATTAAGCCAGCAACTGACCAACGA 2614
 Db 2161 CTTTAAAGCTGTGAAGAGAGACAGAAATGATTAAGCCAGCAACTGACCAACGA 2220
 QY 2615 CTGTACATGATGATGAGGAGCTGTGCAATGAGTCCCTCCAGAGCAACGTTCAAG 2674
 Db 2221 CTGTACATGATGATGAGGAGCTGTGCAATGAGTCCCTCCAGAGCAACGTTCAAG 2280
 QY 2675 CAGTTGGTAGAAGACTTGGATGCAATTTCTCACTGCAACCAATGAG 2722
 Db 2281 CAGTTGGTAGAAGACTTGGATGCAATTTCTCACTGCAACCAATGAG 2328

RESULT 11
 US-08-471-570-7
 ; Sequence 7, Application US/08471570
 ; Patent No. 5750371
 ; GENERAL INFORMATION:
 ; APPLICANT: IGARASHI, Koichi
 ; APPLICANT: SENOO, Masaharu
 ; APPLICANT: WATANABE, Takeya
 ; TITLE OF INVENTION: PROTEIN, DNA AND USE THEREOF
 ; NUMBER OF SEQUENCES: 18
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: DAVID G. CONLIN, DIKE, BRONSTEIN, ROBERTS &
 ; ADDRESSEE: CUSHMAN
 ; STREET: 130 Water Street
 ; CITY: Boston
 ; STATE: Massachusetts
 ; COUNTRY: US
 ; ZIP: 02109
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/471,570
 ; FILING DATE: 06-JUN-1995
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/149,664

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FILING DATE:
APPLICATION NUMBER: US 07/743369
FILING DATE: 16-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: LINEK, Ernest V
REGISTRATION NUMBER: 29822
REFERENCE/DOCKET NUMBER: 40897
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 523-3400
TELEFAX: (617) 523-6440
TELEX: 200291 STRE UR
INFORMATION FOR SEO ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 2676 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 25..2331
US-08-471-570-7

Query Match      74.7% Score 2320; DB 2; Length 2676;
Best Local Similarity 99.8% Pred. No. 0;
Matches 2323; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 395 GACACCGGGGATTGGTACCGGTACCATGTGTCAGCTGGGGGTGTTTCACTGCTGTCGTG 454
DB 1 GACACCGGGGATTGGTACCGGTACCATGTGTCAGCTGGGGGTGTTTCACTGCTGTCGTG 60
QY 455 GTTACCATGTCACCTTTGTCTCTGCGCCCGGCTCTTCACTTGAAGTATACCA 514
DB 61 GTTACCATGTCACCTTTGTCTCTGCGCCCGGCTCTTCACTTGAAGTATACCA 120
QY 515 TTAGAGCGAGAAGAGCCACCAACCAATACCAATCTCTCAACAGAGTACGTGCT 574
DB 121 TTAGAGCGAGAAGAGCCACCAACCAATACCAATCTCTCAACAGAGTACGTGCT 180
QY 575 GCGCCAGGGGAGTCTGTAGAGTGTGCGCTGCTGTTGAAGAGTCCGCGGTATCA 634
DB 181 GCGCCAGGGGAGTCTGTAGAGTGTGCGCTGCTGTTGAAGAGTCCGCGGTATCA 240
QY 635 ACTAAGAGTGGGTGCACTTTGGGGCCCAACATAGACAGTCTTATTTGGGAGTACT 694
DB 241 ACTAAGAGTGGGTGCACTTTGGGGCCCAACATAGACAGTCTTATTTGGGAGTACT 300
QY 695 CAGATTAAGGGGCGCACCTAGAGACTCGGGCTCTATGCTTGTACTGTCAGTGGACT 754
DB 301 CAGATTAAGGGGCGCACCTAGAGACTCGGGCTCTATGCTTGTACTGTCAGTGGACT 360
QY 755 GTAGACAGTGAATCTTGTAATTCATGTGATATGTCAAGATGCAATCTCATCCGAGAT 814
DB 361 GTAGACAGTGAATCTTGTAATTCATGTGATATGTCAAGATGCAATCTCATCCGAGAT 420
QY 815 GATGAGATGACACCGATGTGTGGGAAGATTTTGTCACTGAGAACAGTAAACAAGAGA 874
DB 421 GATGAGATGACACCGATGTGTGGGAAGATTTTGTCACTGAGAACAGTAAACAAGAGA 480
QY 875 GCAACCTACTGACCAACAGAAAGATGAAAGAGGGCTCCATGTGTGCTGCGGCC 934
DB 481 GCAACCTACTGACCAACAGAAAGATGAAAGAGGGCTCCATGTGTGCTGCGGCC 540
QY 935 AACACTGTCAAGTTTCTGCTCCAGCGCGGGGAGAACCAATGCGCAACATGCGGTGCTG 994
DB 541 AACACTGTCAAGTTTCTGCTCCAGCGCGGGGAGAACCAATGCGCAACATGCGGTGCTG 600
QY 995 AAAAAACGGGAAGAGTTTAAAGCAGAGACATGCACTTGAAGCTTAAAGGTAACGAAC 1054
DB 601 AAAAAACGGGAAGAGTTTAAAGCAGAGACATGCACTTGAAGCTTAAAGGTAACGAAC 660
QY 1055 CACTGAGCTCATTTATGAAAGTGTGCTCCATCTGACAAGGGAATTTATCTGTGTA 1114

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DB 661 CACTGAGCTCATTTATGAAAGTGTGCTCCATCTGACAAAGGAATTTATCTGTG 720
QY 1115 GTGGAATGATATAGGGGTCCATCATCAACGTAACCACTGGATTTGAGCGATCG 1174
DB 721 GTGGAATGATATAGGGGTCCATCATCAACGTAACCACTGGATTTGAGCGATCG 780
QY 1175 CCTCACCGGCCCATCTCCAAACCGGACTGCGGCAATGCTCCACAGTGTGAGAGA 1234
DB 781 CCTCACCGGCCCATCTCCAAACCGGACTGCGGCAATGCTCCACAGTGTGAGAGA 840
QY 1235 GACGTAGATTGTCTGCAAGTTTACAGTATGCCACGCCCACTCACTCAAGTATCAG 1294
DB 841 GACGTAGATTGTCTGCAAGTTTACAGTATGCCACGCCCACTCACTCAAGTATCAG 900
QY 1295 CACGTGGAATAAGACGCAATTAACGGGCGGACGGCTGCCACTCAAGTTCTC 1354
DB 901 CACGTGGAATAAGACGCAATTAACGGGCGGACGGCTGCCACTCAAGTTCTC 960
QY 1355 AAGCACTCGGGATTAATAGTTCCAAATGCAAGAGTGTGCTCTGTTCAATGTGACGAG 1414
DB 961 AAGCACTCGGGATTAATAGTTCCAAATGCAAGAGTGTGCTCTGTTCAATGTGACGAG 1020
QY 1415 GCGGATGCTGGGAAATATATATATAGTCTCCAAATATATAGGCGAGGCCAACAGTCT 1474
DB 1021 GCGGATGCTGGGAAATATATATATAGTCTCCAAATATATAGGCGAGGCCAACAGTCT 1080
QY 1475 GCTGCTCACTGTCTCTGCAAAACAGAGCGGCTGGAAAGAAAGGATTAACAGCT 1534
DB 1081 GCTGCTCACTGTCTCTGCAAAACAGAGCGGCTGGAAAGAAAGGATTAACAGCT 1140
QY 1535 TCCCGAGACTACCTGGAGATACCAATTTACTGATAGGGGTCTTCTTAATGCTGTATG 1594
DB 1141 TCCCGAGACTACCTGGAGATACCAATTTACTGATAGGGGTCTTCTTAATGCTGTATG 1200
QY 1595 GTGTAAACAGTACTCTGTGCGGAATGAAGAACAGACCAAGACCAAGCTTCAAGAC 1654
DB 1201 GTGTAAACAGTACTCTGTGCGGAATGAAGAACAGACCAAGACCAAGCTTCAAGAC 1260
QY 1655 CAGCGGCTGTGCAAGGTGACCAAGCTATCCCTCGGAGAGAGGATTAAGTTG 1714
DB 1261 CAGCGGCTGTGCAAGGTGACCAAGCTATCCCTCGGAGAGAGGATTAAGTTG 1320
QY 1715 GCTGATGCACTCTCCATGAACTCCAAACACCCGCTGTGAGTAAACAACGCTTC 1774
DB 1321 GCTGATGCACTCTCCATGAACTCCAAACACCCGCTGTGAGTAAACAACGCTTC 1380
QY 1775 TCTTCAACGGCAGACACCCCATGTGCGAGGGGTCTCCAGTATGAATTCAGAGGAC 1834
DB 1381 TCTTCAACGGCAGACACCCCATGTGCGAGGGGTCTCCAGTATGAATTCAGAGGAC 1440
QY 1835 CCAAAATGGGAATTTCCAAAGATTAAGTGAACCTGGGCAAGCCCTGGGAGAGGTTGC 1894
DB 1441 CCAAAATGGGAATTTCCAAAGATTAAGTGAACCTGGGCAAGCCCTGGGAGAGGTTGC 1500
QY 1895 TTTGGGCAAGTGTCTATGCGGAGAGAGTGGAAATTGACAAAGACCAAGGAGGCG 1954
DB 1501 TTTGGGCAAGTGTCTATGCGGAGAGAGTGGAAATTGACAAAGACCAAGGAGGCG 1560
QY 1955 GTCAACGTGGCGGTGAAGATGTTGAAGATGATGCCAGAGAAAGACCTTCTGATCTG 2014
DB 1561 GTCAACGTGGCGGTGAAGATGTTGAAGATGATGCCAGAGAAAGACCTTCTGATCTG 1620
QY 2015 GTGTCAAGATGGAATGATTAAGATTAAGATTTGGGAAACAAGAAATATCAATCTTCT 2074
DB 1621 GTGTCAAGATGGAATGATTAAGATTAAGATTTGGGAAACAAGAAATATCAATCTTCT 1680
QY 2075 GAGCTTGACACAGAGTGGGCTCTATGTCATATGATGATGCTCTAAAGGCAAC 2134
DB 1681 GAGCTTGACACAGAGTGGGCTCTATGTCATATGATGATGCTCTAAAGGCAAC 1740
QY 2135 CTCGAGAAATACCTCGAGCTCGGAGGCAACCCGGAGTGAAGTACTCTATGACATTAAC 2194
DB 1741 CTCGAGAAATACCTCGAGCTCGGAGGCAACCCGGAGTGAAGTACTCTATGACATTAAC 1800

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; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (595)...(2643)
US-09-954-556-23

Query Match      66.7%; Score 2072.2; DB 3; Length 3025;
Best Local Similarity 89.2%; Pred. No. 0;
Matches 2430; Conservative 0; Mismatches 13; Indels 280; Gaps 7;

Qy 1 CCCCGAGCAAAAGTTGGTGAAGGCAAG-CAAGCTGAGTCTTTCTTCTCTCTCC 59
Db 170 CTCGGAGCAAAAGTTGGTGAAGGCAAGCCAAAGCTGAGTCTTTCTTCTCTCTCC 229
Qy 60 CCAATTCGAGGGGAGCCCGGGGGGCGTATG--GCGCTCTCCGAGCTTGAGGTAAGC 116
Db 230 CCAATTCGAGGGGAGCCCGGGGGGCGTATGCGCGGCTCTCTCCGAGCTTGAGGTAAGC 289
Qy 117 GTGAAGCCCGGAGGCTTGCGCGCCGCGGAGAACCCAGAGACCACTTTCTGCTTGGAG 176
Db 290 GTGAAGCCCGGAGGCTTGCGCGCCGCGGAGAACCCAGAGACCACTTTCTGCTTGGAG 349
Qy 177 TTGCTCCCGCAACCCCGGAGCTTGCTGCTTTCTCATCCCAACCGCGGGGCG-CGGG 235
Db 350 TTGCTCCCGCAACCCCGGAGCTTGCTGCTTTCTCATCCCAACCGCGGGGCGCGGGG 409
Qy 236 ACAACAGAGTGGCGGAGGAGGCTTGCCATTCAAGTACTGAGAGAGAGC-GCAGCGCC 294
Db 410 ACAACAGAGTGGCGGAGGAGGCTTGCCATTCAAGTACTGAGAGAGAGCGCGCGCC 469
Qy 295 TCGGTTCTGAGCCCAACCGCA-GCTGAAGGCAATGCGCGTGAATGCATGCGGTAGAGAA 353
Db 470 TCGGTTCTGAGCCCAACCGCAGCTGAAGGCAATGCGCGTGAATGCATGCGGTAGAGAA 529
Qy 354 GTGTGAGATGGGATTAAGTCTCAATGAGATATGAGAAAGAGAACCGGGGATTTGTAACG 413
Db 530 GTGTGAGATGGGATTAAGTCTCAATGAGATATGAGAAAGAGAACCGGGGATTTGTAACG 589
Qy 414 TAAACATGAGTGAAGTGGGGTCTGTTTCATCTGCTGGTCTGAGTCAACATGAGCACTTGT 473
Db 590 TAAACATGAGTGAAGTGGGGTCTGTTTCATCTGCTGGTCTGAGTCAACATGAGCACTTGT 649
Qy 474 CCGTGGCCCGGCGCTCTCTTCAAGTTTAAAGTGAAGATACCAATTAAAGCCAAAGCCAC 533
Db 650 CCGTGGCCCGGCGCTCTCTTCAAGTTTAAAGTGAAGATACCAATTAAAGCCACGA----- 701
Qy 534 CAACCAATATCAAAATCTCTCAACAGAAAGTGAAGTGGCTGGCCAGGGGAGTGGCTAG 593
Db 702 ----- 701
Qy 594 AGGTGGCTGCTGTTGAAGAGTCCGCGGTGATCAGTTGACTAAGATGGGGTGGACT 653
Db 702 ----- 701
Qy 654 TGGGGCCCAACATAGAGAGAGTCTTATTTGGGGAGTACTTGAGATAAAGGCGCCACAC 713
Db 702 ----- 701
Qy 714 CTAGAGACTCCGGCTCTATGCTTGTATGTCAGTAGAGACTGTAGACAGTAAACTTGGT 773
Db 702 ----- 701
Qy 774 ACTTCAATGTAATGTCCAGATGCATCTCATCCGAGATGATGAGATGACCCGATG 833
Db 702 -----AGATGCATCTCATCCGAGATGATGAGATGACCCGATG 742
Qy 834 GTGCGGAAGATTTTGTCAGTGAGAACATTAACAAGAGAGACCAATCTGAGCAACA 893
Db 743 GTGCGGAAGATTTTGTCAGTGAGAACATTAACAAGAGAGACCAATCTGAGCAACA 802
Qy 894 CAGAAAAGATGAAAAGCGGCTCATGCTGTGCTGGCCCACTGTTCACAACTTTCCT 953
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Db 803 CAGAAAAGATGAAAAGCGGCTCATGCTGTGCGGCCCAACTGTCAAGTTTCCT 862
Qy 954 GCCCAGCCGGGGGAAACCCATATGCCAATTCGGGTGGCTGAAAAAGGAAAGATTTA 1013
Db 863 GCCCAGCCGGGGGAAACCCATATGCCAATTCGGGTGGCTGAAAAAGGAAAGATTTA 922
Qy 1014 AGCAGAGACATTCGATTTGGAGGGCTCAAGAGTACGAACCAAGCATCTGAGCTCATATGG 1073
Db 923 AGCAGAGACATTCGATTTGGAGGGCTCAAGAGTACGAACCAAGCATCTGAGCTCATATGG 982
Qy 1074 AAGTGTGTCCCATCTGACAAAGGAAATTATACCTGTGTATGAGATGATATACGGGT 1133
Db 983 AAGTGTGTCCCATCTGACAAAGGAAATTATACCTGTGTGTGAGAAATGAAATACGGGT 1042
Qy 1134 CCATCAATCAACATGACCTGGAATGTTGTGAGCGCATGCGCTCACCGGCCCCATCTCC 1193
Db 1043 CCATCAATCAACATGACCTGGAATGTTGTGAGCGCATGCGCTCACCGGCCCCATCTCC 1102
Qy 1194 AAGCGGAGCTGGCCAAATGCTTCCAGAGTTCGAGAGAGACGTAGAGTTTGTCTGCA 1253
Db 1103 AAGCGGAGCTGGCCAAATGCTTCCAGAGTTCGAGAGAGACGTAGAGTTTGTCTGCA 1162
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Db 1583 TGAACCAACGTAATCCCCCTGGGAGAGACAG-----GTTTGGCTGAGTCAAGCTCTGCA 1636
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Qy 1914 CGGAAGAGTGGGAATTTGCAAAAGCAAGCCCAAGAGAGCGGTCAACGTTGCGCTGAAGA 1973
Db 1817 CGGAAGAGTGGGAATTTGCAAAAGCAAGCCCAAGAGAGCGGTCAACGTTGCGCTGAAGA 1876
Qy 1974 TGTGAAAGATGATCCACAGAAAGACCTTTCATCTGATCTGATCTGAGATGAGATGA 2033
Db 1877 TGTGAAAGATGATCCACAGAAAGACCTTTCATCTGATCTGATCTGAGATGAGATGA 1936
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QY 2034 TGAAGATGATGGGAAACACAGAAATATCAATAATCTTCTGGAGGCTGACACAGAGATG 2093
DB 1937 TGAAGATGATGGGAAACACAGAAATATCAATAATCTTCTGGAGGCTGACACAGAGATG 1996
QY 2094 GGCCTCTATGTCATAGTTGATGATGCTCTTAAAGGCAACCTCCAGAAATACCTCCGAG 2153
DB 1997 GGCCTCTATGTCATAGTTGATGATGCTCTTAAAGGCAACCTCCAGAAATACCTCCGAG 2056
QY 2154 CCCGAGGCCACCCGGGATGAGTACTCTTATGACATTTAACCGTGTCTTCTGAGAGACAG 2213
DB 2057 CCCGAGGCCACCCGGGATGAGTACTCTTATGACATTTAACCGTGTCTTCTGAGAGACAG 2116
QY 2214 TGAACCTTCAAGAGCTTGATGTCATGACCTTACCAAGCTGGCCAGACGAGAGTACTCTTG 2273
DB 2117 TGAACCTTCAAGAGCTTGATGTCATGACCTTACCAAGCTGGCCAGACGAGAGTACTCTTG 2176
QY 2274 CTTCACCAAAATGATTCATGAGATTTAGCAGCCAGAAATGTTTGTGTAACAGAAAC 2333
DB 2177 CTTCACCAAAATGATTCATGAGATTTAGCAGCCAGAAATGTTTGTGTAACAGAAAC 2236
QY 2334 ATGTGATGAAATATAGCAGCTTGTGACTGCGCAGAGATTAACAATATATGACTATTACA 2393
DB 2237 ATGTGATGAAATATAGCAGCTTGTGACTGCGCAGAGATTAACAATATATGACTATTACA 2296
QY 2394 AAAAGACCAACATGGCGGCTTCCAGTCAAGTGGTCCAGAAAGCCCTGTGTA 2453
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DB 2357 GAGTATTAACCTCAATGAGATGTCGTCTTCCGGGGGTGTAATGTGGAGATCTTCA 2416
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QY 2634 ACTGTGGCATGAGAGTCCCTCCCAAGACCAAGTTCAGAGAGTGTGTAAGAGACTTG 2693
DB 2537 ACTGTGGCATGAGAGTCCCTCCCAAGACCAAGTTCAGAGAGTGTGTAAGAGACTTG 2596
QY 2694 ATCGAATTCCTACTCTCAACAC 2716
DB 2597 ATCGAATTCCTCCCAACCTCTCC 2619

RESULT 14
US-08-471-570-5
; Sequence 5, Application US/08471570
; Patent No. 5750371
; GENERAL INFORMATION:
; APPLICANT: IGARASHI, Koichi
; APPLICANT: SENOO, Masaharu
; APPLICANT: WATANABE, Tatsuya
; TITLE OF INVENTION: PROTEIN, DNA AND USE THEREOF
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DAVID G. CONLIN, DIKE, BRONSTEIN, ROBERTS &
; ADDRESSER: CUSHMAN
; STREET: 130 Water Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: US
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25

;/ CURRENT APPLICATION DATA:
;/ APPLICATION NUMBER: US/08/471,570
;/ FILING DATE: 06-JUN-1995
;/ CLASSIFICATION: 435
;/ PRIOR APPLICATION DATA:
;/ APPLICATION NUMBER: US/08/149,664
;/ FILING DATE:
;/ APPLICATION NUMBER: US 07/743369
;/ FILING DATE: 16-AUG-1991
;/ ATTORNEY/AGENT INFORMATION:
;/ NAME: LINEK, Ernest V
;/ REGISTRATION NUMBER: 29822
;/ REFERENCE/DOCKET NUMBER: 40897
;/ TELECOMMUNICATION INFORMATION:
;/ TELEPHONE: (617)523-3400
;/ TELEFAX: (617)523-6440
;/ TELEX: 200291 STR UR
;/ INFORMATION FOR SEQ ID NO: 5:
;/ SEQUENCE CHARACTERISTICS:
;/ LENGTH: 1954 base pairs
;/ TYPE: nucleic acid
;/ STRANDEDNESS: double
;/ TOPOLOGY: linear
;/ MOLECULE TYPE: cDNA
;/ FEATURE:
;/ NAME/KEY: CDS
;/ LOCATION: 25..1953
;/ US-08-471-570-5

Query Match 62.7%; Score 1946; DB 2; Length 1954;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1949; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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DB 61 GTACACATGGGCAACCTTGTCCCTGGCCGGCCCTCCTTCACTTGTGATGAGATACACA 120
QY 515 TTAGAGCCAGAAAGAGCCACCAACCAATCTCTCAACCAAGTGTACGTGGCT 574
DB 121 TTAGAGCCAGAAAGAGCCACCAACCAATCTCTCAACCAAGTGTACGTGGCT 180
QY 575 GCGCCAGGGAGTCCGTAGAGTGGCTGCTGCTGTTGAAGAGTCCGCTGATCACTTGG 634
DB 181 GCGCCAGGGAGTCCGTAGAGTGGCTGCTGCTGTTGAAGAGTCCGCTGATCACTTGG 240
QY 635 ACTAAGGATGGGGTGTGACTTGGGGCCCAACATAGGACAGTGTATGAGGAGTACTTG 694
DB 241 ACTAAGGATGGGGTGTGACTTGGGGCCCAACATAGGACAGTGTATGAGGAGTACTTG 300
QY 695 CAGATTAAGGGGCGCAACCTTAGAGCTCCGCTCTATGCTTGTACTGCCAGTAGACT 754
DB 301 CAGATTAAGGGGCGCAACCTTAGAGCTCCGCTCTATGCTTGTACTGCCAGTAGACT 360
QY 755 GTAGACATGAACTTGTGTAATCTCATGTGTAATGTCAAGATGCCATCTCATCCGAGAT 814
DB 361 GTAGACATGAACTTGTGTAATCTCATGTGTAATGTCAAGATGCCATCTCATCCGAGAT 420
QY 815 GATGAGATGACACCGATGCTGGGAGATTTTGTCAAGTGAACAGTAAACAAGAGA 874
DB 421 GATGAGATGACACCGATGCTGGGAGATTTTGTCAAGTGAACAGTAAACAAGAGA 480
QY 875 GCAACATATGACCAACAAGAAAAAGATGAAAAAGCGCTCATGCTGTGCTGGGCT 934
DB 481 GCAACATATGACCAACAAGAAAAAGATGAAAAAGCGCTCATGCTGTGCTGGGCT 540
QY 935 AACACTGTCAAGTTTGTGCTGCCAGCGGGGGGAAACCCATGCAACATGCGGTGGCTG 994
DB 541 AACACTGTCAAGTTTGTGCTGCCAGCGGGGGGAAACCCATGCAACATGCGGTGGCTG 600

QY	995	AAAAACGGGAAGAGCTTTAAAGCAGAGCATGCGATTGGAGGCTTACAGGTATCCGAACACAG	1054
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QY	1055	CACGTGAGCCCTCATTTATGAGAAAGTGTGCTCCATCTGTGCAAGGGAAATTTATCTGTGTGA	1114
Db	661	CACGTGAGCCCTCATTTATGAGAAAGTGTGCTCCATCTGTGCAAGGGAAATTTATCTGTGTG	720
QY	1115	GTGAGAAATGAAATCGGGTCCATCATCAATCAACGTACCACTTGATGTTGTGAGCGATCG	1174
Db	721	GTGAGAAATGAAATCGGGTCCATCATCAACGTACCACTTGATGTTGTGAGCGATCG	780
QY	1175	CCTCAACCGGCCCATCTCTCCAAAGCCGGAGATGCGCGGCAAAATGCTCTCCACAGTGTGTGGAGA	1234
Db	781	CCTCAACCGGCCCATCTCTCCAAAGCCGGAGATGCGCGGCAAAATGCTCTCCACAGTGTGTGGAGA	840
QY	1235	GACGTGAGGTTTGTGTGCAAGGTTTACAGTATGTCGAGCCCAATCCAGTGTGATCAAG	1294
Db	841	GACGTGAGGTTTGTGTGCAAGGTTTACAGTATGTCGAGCCCAATCCAGTGTGATCAAG	900
QY	1295	CACGTGAAAAAGAACGGCAGTAAATATACGGGCCCGACGGGGCTGCCCTACCTCAAGTTCTC	1354
Db	901	CACGTGAAAAAGAACGGCAGTAAATATACGGGCCCGACGGGGCTGCCCTACCTCAAGTTCTC	960
QY	1355	AAGCACTCGGGAGTAATATGTTCCATGCAAGATGCTGCTGTTCATATGTACCGAG	1414
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QY	1415	GGGAGTCTGGGGAAATATATATGTAAGTCTCCATTTATATAGGGCAGGCCAACAGCT	1474
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QY	1475	GCCTGGCTCACTGTCTCTGCAAAACAGCAAGCCTGTGAAAGAAAGAAAGATTACA	1534
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QY	1535	TCCCAAGACTACTCGTAGATACCTTTAATCTGCAATAGGGGCTTTTATATGGCTGTATG	1594
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QY	1595	GTGGTAACAGTACTCTGTGCGGAATGAAAGAACAGACCAAGAAACCGACCTTACAGCAGC	1654
Db	1201	GTGGTAACAGTACTCTGTGCGGAATGAAAGAACAGACCAAGAAACCGACCTTACAGCAGC	1260
QY	1655	CAGCCGGCTGTCAACAGCTGACCAAAACGTATCCCCCTGTGCGAGACAGGTAAACGTTTCG	1714
Db	1261	CAGCCGGCTGTCAACAGCTGACCAAAACGTATCCCCCTGTGCGAGACAGGTAAACGTTTCG	1320
QY	1715	GCTGAGTCAAGCTCTCTCATGAACTTCCAAACCCCGCTGTGTGAGATTAACAACGCTTC	1774
Db	1321	GCTGAGTCAAGCTCTCTCATGAACTTCCAAACCCCGCTGTGTGAGATTAACAACGCTTC	1380
QY	1775	TCTTGAACGGCAGACACCCCAATGCTGGAGAGGGGTCTCGAATATGAACCTTCCAGAGAC	1834
Db	1381	TCTTGAACGGCAGACACCCCAATGCTGGAGAGGGGTCTCGAATATGAACCTTCCAGAGAC	1440
QY	1835	CCAAATATGGAGATTTCACAGAGATTAAGTGAACCTGTGGCAACCCCTGTGGAGAGATTTC	1894
Db	1441	CCAAATATGGAGATTTCACAGAGATTAAGTGAACCTGTGGCAACCCCTGTGGAGAGATTTC	1500
QY	1895	TTTGGGCAAGTGTCACTGCGGAAAGCATGGGGAATTTGACAAAGACAGCCCTTCCATGCTG	2014
Db	1501	TTTGGGCAAGTGTCACTGCGGAAAGCATGGGGAATTTGACAAAGACAGCCCTTCCATGCTG	1620
QY	1955	GTCAACCTGTGCGCTGAAGATGTTGAAAGATGATCCACAGAAAGACCTTCTCATGCTG	2074
Db	1561	GTCAACCTGTGCGCTGAAGATGTTGAAAGATGATCCACAGAAAGACCTTCTCATGCTG	1680
QY	2015	GTGTCAAGATGAGATGATGAAGATGATTGGGAAACAAAGAAATATCATTAATCTTCTT	2074
Db	1621	GTGTCAAGATGAGATGATGAAGATGATTGGGAAACAAAGAAATATCATTAATCTTCTT	1680
QY	2075	GGAGCTTGACACAGAGTGGGCTCTTATGTCAATATGTTAGTATGCTTAAAGCAAC	2134

Accession	Sequence	Length
Db	1661 GGAGCTGTCACACAGATGGGCTCTCATGTCAATGTTGAGTATGGCTCTTAAGGCGAAC	1740
Qy	2135 CTCGGAGAAATCTCCACAGCCCGGAGGCAACCGGAGATGAGTACTCTATGACATTAC	2194
Db	1741 CTCGGAGATACCTTCGAGCCCGAGGCGACCCGGATGAGTACTCTATGACATTAC	1800
Qy	2195 CGTGTCTCTGAGAGCAGATGACCTTCAGGACTTGGTGTATGCACTTACAGCTGGCC	2254
Db	1801 CGTGTCTCTGAGAGCAGATGACCTTCAGGACTTGGTGTATGCACTTACAGCTGGCC	1860
Qy	2255 AGACGATGAGATCTTGGCTTCCCAAAATGTATTCAATCGAGATTTAGCAGCAGAAAT	2314
Db	1861 AGAGCATGAGATCTTGGCTTCCCAAAATGTATTCAATCGAGATTTAGCAGCAGAAAT	1920
Qy	2315 GTTTTGGTAAACGAAAAATATGTATGATAAAATAG	2348
Db	1921 GTTTTGGTAAACGAAAAATATGTATGATAAAATAG	1954

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/ RESULT 15
/ US-09-949-016-3171
/ Sequence 3171, Application US/09949016
/ Patent No. 6812339
/ GENERAL INFORMATION:
/ APPLICANT: VENTER, J. Craig et al.
/ TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
/ TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
/ FILE REFERENCE: CLO01307
/ CURRENT APPLICATION NUMBER: US/09/949,016
/ CURRENT FILING DATE: 2000-04-14
/ PRIOR APPLICATION NUMBER: 60/241,755
/ PRIOR FILING DATE: 2000-10-20
/ PRIOR APPLICATION NUMBER: 60/237,768
/ PRIOR FILING DATE: 2000-10-03
/ PRIOR APPLICATION NUMBER: 60/231,498
/ PRIOR FILING DATE: 2000-09-08
/ NUMBER OF SEQ ID NOS: 207012
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 3171
/ LENGTH: 2079
/ TYPE: DNA
/ ORGANISM: Human
/ US-09-949-016-3171

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Best Local Similarity	96.1%;	Pred. No. 0;		
Matches 1998; Conservative	0;	Mismatches 61;	Indels 21;	Gaps 5

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Db	69	TCCGCGTATCATGCCCCGTAGAGGAAAGTGTCAAGTGGGATTTAAACGTCCACATGAGAT	128
QY	387	ATGGAAGAAGACCGGGGATTGGTACCGGTACCATGGTCAAGTGGGGTCGTTTCATCTGCC	446
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QY	447	TGGTGGTGCACCATGGCAACCTTGTCCCTGGCCCCGGCCCTTCCTCACTTAAAGTTGAAG	506
Db	189	TGGTGGTGCACCATGGCAACCTTGTCCCTGGCCCCGGCCCTTCCTCACTTAAAGTTGAAG	248
QY	507	ATACCACTTAAAGCCAGAAGACCAACAACAATATTCCTCAACCAAGAAGTGT	566
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QY	567	ACGTGGCTCGCCAGGGGAGTGGCTTAGAGGTGGCTGCTTTGTAAGAAATGGCCCGCTGA	626
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 DB 1209 TATCTTTTCACTGTGATGTGATGACAGTTCTGCC-----AGCGCTGGAAGAAA 1259
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 DB 1740 AAGAAGCTTTCATCTGAGTGTGATGAGATGAGATGAGATGAGATGAGATGAGATGAG 1799
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OM nucleic - nucleic search, using sw model

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Gapop 10.0 , Gapext 1.0

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Total number of hits satisfying chosen parameters: 37784340

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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3013.2	97.0	4574	8 US-10-648-593-132	Sequence 132, App
2	3013.2	97.0	4574	10 US-10-956-157-2419	Sequence 2419, App
3	3013.2	97.0	4574	12 US-10-960-414-1172	Sequence 172, App
4	3013.2	97.0	4574	13 US-11-019-829-39	Sequence 39, App
5	3013.2	97.0	4574	16 US-11-072-175-1132	Sequence 132, App
6	2904.2	93.5	4587	13 US-11-019-829-38	Sequence 38, App
7	2849.4	91.7	4575	13 US-11-019-829-42	Sequence 42, App
8	2806.2	90.3	3080	3 US-09-954-556-25	Sequence 25, App
9	2781.8	89.6	4268	3 US-09-954-456-293	Sequence 293, App
10	2781.8	89.6	4268	3 US-09-954-456-1599	Sequence 1599, App
11	2781.8	89.6	4268	3 US-09-954-556-3	Sequence 3, App
12	2781.8	89.6	4268	3 US-09-968-007A-461	Sequence 461, App
13	2781.8	89.6	4268	10 US-10-843-641A-3320	Sequence 3320, App
14	2781.8	89.6	4268	10 US-10-843-641A-4626	Sequence 4626, App
15	2781.8	89.6	4268	10 US-10-843-641A-6931	Sequence 6931, App
16	2747.4	88.5	4667	7 US-10-007-926A-15	Sequence 15, App
17	2747.4	88.5	4667	13 US-11-019-829-47	Sequence 47, App

18	2747.4	88.5	4666	9 US-10-723-860-6953	Sequence 6953, App
19	2728.6	87.8	2923	3 US-09-954-556-20	Sequence 20, App
20	2723.4	87.7	2826	3 US-09-954-556-21	Sequence 21, App
21	2722	87.6	2868	3 US-09-954-556-19	Sequence 19, App
22	2722	87.6	2941	3 US-09-954-556-18	Sequence 18, App
23	2639.6	85.0	3219	13 US-11-019-829-44	Sequence 44, App
24	2556.8	82.3	3248	13 US-10-302-812-43	Sequence 43, App
25	2506	80.7	3216	13 US-11-019-829-43	Sequence 43, App
26	2475	79.7	4310	13 US-11-019-829-45	Sequence 45, App
27	2404.4	77.4	4222	13 US-11-019-829-49	Sequence 49, App
28	2382.4	76.7	4216	13 US-11-019-829-50	Sequence 50, App
29	2350.8	75.7	4305	13 US-11-019-829-48	Sequence 48, App
30	2327.4	74.9	2466	8 US-10-843-339C-85	Sequence 85, App
31	2327.4	74.9	3244	3 US-09-954-556-24	Sequence 24, App
32	2327.4	74.9	3244	3 US-09-954-556-24	Sequence 24, App
33	2327.4	74.9	3244	3 US-09-873-367C-171	Sequence 171, App
34	2327.4	74.9	3244	10 US-10-843-641A-171	Sequence 171, App
35	2327.4	74.9	3244	10 US-10-505-680-715	Sequence 715, App
36	2320	74.7	2650	3 US-11-019-829-40	Sequence 40, App
37	2201	70.9	3306	3 US-09-954-556-10	Sequence 10, App
38	2185	70.3	2672	16 US-11-136-527-3514	Sequence 3514, App
39	2116.2	68.1	3011	10 US-10-956-157-4901	Sequence 4901, App
40	2072.2	66.7	3025	3 US-09-954-556-23	Sequence 23, App
41	1890.4	60.9	2079	6 US-10-087-192-1133	Sequence 1133, App
42	1677.8	54.0	2311	16 US-11-136-527-3513	Sequence 3513, App
43	1475.6	47.5	1978	6 US-10-087-192-1130	Sequence 1130, App
44	1468.4	47.3	1807	13 US-11-019-829-46	Sequence 46, App
45	1345	43.3	1475	3 US-09-954-556-27	Sequence 27, App

ALIGNMENTS

RESULT 1
US-10-648-593-132
; Sequence 132, Application US/10648593
; Publication No. US20040106132A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: IDENTIFICATION OF GENES FOR PREDICTING ACTIVITY OF COMPOUNDS THAT
; TITLE OF INVENTION: INTERACT WITH AND/OR MODULATE PROTEIN TYROSINE KINASES AND/OR
; FILE REFERENCE: D0273 NP
; CURRENT APPLICATION NUMBER: US/10/648,593
; CURRENT FILING DATE: 2003-08-26
; PRIOR APPLICATION NUMBER: 60/406,385
; PRIOR FILING DATE: 2002-08-27
; NUMBER OF SEQ ID NOS: 557
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 132
; LENGTH: 4574
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-648-593-132

Query Match	97.0%;	Score 3013.2;	DB 8;	Length 4574;
Best Local Similarity	99.5%;	Pred. No. 0;		
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			Indels	9;
			Gaps	7;
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/ Sequence 2419, Application US/10956157
/ Publication No. US20050118625A1
/ GENERAL INFORMATION:
/ APPLICANT: Wyeth
/ APPLICANT: Mounts, William
/ TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
/ FILE REFERENCE: HUMAN OSTEOBLASTS AND HUMAN PROTEASES
/ CURRENT FILING DATE: 2004-10-04
/ NUMBER OF SEQ ID NOS: 319805
/ SOFTWARE: Patentin version 3.2
/ SEQ ID NO 2419
/ LENGTH: 4574
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-10-956-157-2419

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Query Match 97.0%; Score 3013.2; DB 10; Length 4574;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 3097; Conservative 0; Mismatches 8; Indels 9; Gaps 7;

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Db      2327 GCGCGGAGGACCGCGGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2386
Qy      2213 ATGACCTTCAAGGACTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2272
Db      2287 ATGACCTTCAAGGACTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2446
Qy      2273 GCTTCCCAAAATGTATTTCAATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2332
Db      2447 GCTTCCCAAAATGTATTTCAATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2506
Qy      2333 AATGTATGAAAATATGAGAGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2392
Db      2507 AATGTATGAAAATATGAGAGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2566
Qy      2393 AAAAAAGCAACAAATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2452
Db      2567 AAAAAAGCAACAAATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2626
Qy      2453 AGACTATATCACTCATGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2512
Db      2627 AGACTATATCACTCATGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2686
Qy      2513 ACTTTAGGGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2572
Db      2687 ACTTTAGGGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2746
Qy      2573 GAAGGACACAGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2632
Db      2747 GAAGGACACAGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2806
Qy      2633 GACGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2692
Db      2807 GACGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2866
Qy      2693 GATGGAATTTCTCACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2752
Db      2867 GATGGAATTTCTCACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2926
Qy      2753 CAGTATTTCACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2812
Db      2927 CAGTATTTCACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2986
Qy      2813 TTTTCTCCAGACCCCAAGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2872
Db      2987 TTTTCTCCAGACCCCAAGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3046
Qy      2873 AGTGTATTAACATGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2932
Db      3047 AGTGTATTAACATGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3106
Qy      2933 AGCTTACTGAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2992
Db      3107 AGCTTACTGAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3166
Qy      2993 GATCAGAGAGATTAATATTTGAAAAGTATGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3052
Db      3167 GATCAGAGAGATTAATATTTGAAAAGTATGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3226
Qy      3053 AAAAATTTGTATTTTCCCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3106
Db      3227 AAAAATTTGTATTTTCCCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3280

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RESULT 3
US-10-960-414-172
; Sequence 172, Application US/10960414
; Publication No. US20060074565A1
; GENERAL INFORMATION:
; APPLICANT: MILLER, LANCE D.
; APPLICANT: GEORGE, JOSEPH
; APPLICANT: VEGA, VINCENTIUS B.
; TITLE OF INVENTION: METHODS, SYSTEMS, AND COMPOSITIONS FOR CLASSIFICATION,
; PROGNOSIS, AND DIAGNOSIS OF CANCERS

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FILE REFERENCE: 38271-76067
CURRENT APPLICATION NUMBER: US/10/960,414
CURRENT FILING DATE: 2004-10-06
NUMBER OF SEQ ID NOS: 500
SOFTWARE: PatentIn version 3.3
SEQ ID NO: 172
LENGTH: 4574
TYPE: DNA
ORGANISM: Homo sapiens
US-10-960-414-172

Query Match 97.0%; Score 3013.2; DB 12; Length 4574;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 3097; Conservative 0; Mismatches 8; Indels 9; Gaps 7;

1 CCCGAGAGCAAGTTGTTGAGGCAACG-CAAGCTGAGTCTTCTCTCTGCTTC 59
168 CTGGGAGAGAAAGTTGGTGGAGGCAAGCGCAAGCTGAGTCTTCTCTCTGCTTC 227
60 CCAATCCGAGGAGAGCCCGCGGCGTCAATG--GGCTCTCTCGAGGCTTGGGTACGC 116
228 CCAATCCGA-GGAGCCCGCGGCGTCAATGCGCGCTCTCTCGAGGCTTGGGTACGC 286
117 G-TGAAGCCCGGAGGCTTGGCGCGGAGAGCCCAAGACCACTCTGAGTTTGA 175
287 GCTGAAGCCCGGAGGCTTGGCGCGGAGAGCCCAAGACCACTCTCTGAGTTTGA 346
176 GTTGTCTCCCGCAACCCCGGCGTCTGCTGCTTCTCCATCCGACCGCGGCGC-CGAG 234
347 GTTGTCTCCCGCAACCCCGGCGTCTGCTGCTTCTCCATCCGACCGCGGCGC-CGAG 406
235 GAACAACAGGTGCGGAGAGGCGTTGCCATTCAAGTGACTGAGAGAGC-GCAGCGC 293
407 GAACAACAGGTGCGGAGAGGCGTTGCCATTCAAGTGACTGAGAGAGCAGCGAGCGC 466
294 CTCGGTCTGAGCCCAACCGCA-GCTGAAGGCAATGCGGCTGATGCGCGCTAGAGA 352
467 CTCGGTCTGAGCCCAACCGCAAGGCTGAAGGCAATGCGGCTGATGCGCGCTAGAGA 526
353 AGTGTGAGATGAGATTAAGTCAATGAGATATGAAGAGACCGGAGATTGGTACC 412
527 AGTGTGAGATGAGATTAAGTCAATGAGATATGAAGAGACCGGAGATTGGTACC 586
413 GTTACATGATGAGTGGGCTGTTCAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 472
587 GTTACATGATGAGTGGGCTGTTCAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 646
473 TCCCTGAGCCCGGCTCTCTCAAGTTAGTGAAGATACCAATTAAGGCAAGAGCA 532
647 TCCCTGAGCCCGGCTCTCTCAAGTTAGTGAAGATACCAATTAAGGCAAGAGCA 706
533 CCAACCAATTAACCAATCTCTCAACAGAGATGATGAGTGGCTGCGCAGAGAGTGGCTA 592
707 CCAACCAATTAACCAATCTCTCAACAGAGATGATGAGTGGCTGCGCAGAGAGTGGCTA 766
593 GAGGTGCGCTGCTGTTGAAGATGCGCGCTGATCAATTGAAGTGAAGTGGGTGCA 652
767 GAGGTGCGCTGCTGTTGAAGATGCGCGCTGATCAATTGAAGTGAAGTGGGTGCA 826
653 TTGGGAGCCCAAGATGAGAGAGTGTATTGGGAGATTAAGTGAAGTGGGTGCA 712
827 TTGGGAGCCCAAGATGAGAGAGTGTATTGGGAGATTAAGTGAAGTGGGTGCA 886
713 CCTAGAGATCTCGGCTCTATGCTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 772
887 CCTAGAGATCTCGGCTCTATGCTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 946
773 TACTTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 832
947 TACTTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1006
833 GGTGGGAGATTTTGTGATGAGAGAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 892

1007 GGTGGGAGATTTTGTGATGAGAGAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1066
893 ACAGAAAGATGAGAAAGAGGCTCCATGCTGAGTGGGCAACAGTCAAGTTGGC 952
1067 ACAGAAAGATGAGAAAGAGGCTCCATGCTGAGTGGGCAACAGTCAAGTTGGC 1126
953 TGCCAGCGGAGGAGAACCAATGCAACATGCGGTGCTGAAAACGGAGAGGTTT 1012
1127 TGCCAGCGGAGGAGAACCAATGCAACATGCGGTGCTGAAAACGGAGAGGTTT 1186
1013 AAGCAGAGCATGCTGATGAGGCTCAAGGATCAAGACCACTGAGGCTCTATG 1072
1187 AAGCAGAGCATGCTGATGAGGCTCAAGGATCAAGACCACTGAGGCTCTATG 1246
1073 GAAATGTGTCCTCACTGAGCAAGGAAATTAATCTGATGATGAGAGATGAATACGG 1132
1247 GAAATGTGTCCTCACTGAGCAAGGAAATTAATCTGATGATGAGAGATGAATACGG 1306
1133 TCCATCAATCAACGTAACCACTGATGTTGAGAGCATGCGCTCAACCGCCATCTC 1192
1307 TCCATCAATCAACGTAACCACTGATGTTGAGAGCATGCGCTCAACCGCCATCTC 1366
1193 CAAGCCGAGCTGCGCAAAATGCTTCAAGTGTGAGAGAGAGTGAAGTTGTCTGC 1252
1367 CAAGCCGAGCTGCGCAAAATGCTTCAAGTGTGAGAGAGAGTGAAGTTGTCTGC 1426
1253 AAGTTTACATGATGCTGAGGCTCAAGTGTGAGAGAGAGTGAAGTTGTCTGC 1312
1427 AAGTTTACATGATGCTGAGGCTCAAGTGTGAGAGAGAGTGAAGTTGTCTGC 1486
1313 AGTAATATGAGGCGCGAGCGGCTGCTCAAGTGTGAGAGAGTGAAGTTGTCTGC 1372
1487 AGTAATATGAGGCGCGAGCGGCTGCTCAAGTGTGAGAGAGTGAAGTTGTCTGC 1546
1373 AGTTCAATGCAAGAGTGTGCTGTTCAATGATGAGAGAGAGTGAAGTTGTCTGC 1432
1547 AGTTCAATGCAAGAGTGTGCTGTTCAATGATGAGAGAGAGTGAAGTTGTCTGC 1606
1433 AATGTAAGTGTGCAATTAATTAAGGAGAGAGAGTGAAGTTGTCTGC 1492
1607 AATGTAAGTGTGCAATTAATTAAGGAGAGAGAGTGAAGTTGTCTGC 1666
1493 CCAAAACAG 1552
1667 CCAAAACAG 1726
1553 AATGCAATTAATGATGAGGCTCTTCAATGCTGATGAGAGAGAGTGAAGTTGTCTGC 1612
1727 AATGCAATTAATGATGAGGCTCTTCAATGCTGATGAGAGAGAGTGAAGTTGTCTGC 1786
1613 TGCCAGATGAG 1672
1787 TGCCAGATGAG 1846
1673 CTGACCAACGATGCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1732
1847 CTGACCAACGATGCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1906
1733 ATGAATCTCAACAGCCCGTGTGATGAGATTAACAGCTCTTCAACGAGAGAG 1792
1907 ATGAATCTCAACAGCCCGTGTGATGAGATTAACAGCTCTTCAACGAGAGAG 1966
1793 CCAATGCTGAGAGGCTCTGAGATGAGATTAACAGCTCTTCAACGAGAGAG 1852
1967 CCAATGCTGAGAGGCTCTGAGATGAGATTAACAGCTCTTCAACGAGAGAG 2026
1853 AAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1912
2027 AAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2086
1913 GCGAG 1972
2087 GCGAG 2146

QY	1973	ATGTTGAAAGTATGATGCCACAGAGAAAGACCTTTCGATCTCGATGTCAGAGATGGAGATG	2032
Db	2147	ATGTTGAAAGATGATGCGCACAGAGAAAGACCTTTCGATCTCGATGTCAGAGATGGAGATG	2206
QY	2033	ATGAAGATGATGTGGGAAACACAAGAAATATCATAAATCTTCTTGAGCCTGACACAGAT	2092
Db	2207	ATGAAGATGATGTGGGAAACACAAGAAATATCATAAATCTTCTTGAGCCTGACACAGAT	2266
QY	2093	GGGCTCTCTATGTCATATGTTGAATATGCTCTTAAAGGCAACTCCGAGAAATCCCTCCGA	2152
Db	2267	GGGCTCTCTATGTCATATGTTGAATATGCTCTTAAAGGCAACTCCGAGAAATCCCTCCGA	2326
QY	2153	GCCGGAGGCGCACCCGGGATGGAGTACTCCATATGACATTTAAACCGTGTCTCTGAGGACAG	2212
Db	2327	GCCGGAGGCGCACCCGGGATGGAGTACTCCATATGACATTTAAACCGTGTCTCTGAGGACAG	2386
QY	2213	ATGACCTTCAAGAGACTTGATGTCATGACCTTCAAGCTGCGCAGACGATGAGATCTTG	2272
Db	2387	ATGACCTTCAAGAGACTTGATGTCATGACCTTCAAGCTGCGCAGACGATGAGATCTTG	2446
QY	2273	GCTTCCCAAAATATGATTAATTCAGATTTTGACGACCGAAGATGTTTGTATGACAGAAAC	2332
Db	2447	GCTTCCCAAAATATGATTAATTCAGATTTTGACGACCGAAGATGTTTGTATGACAGAAAC	2506
QY	2333	AATGTGATGAAATATGACAGACTTTGGACTGCGCCAGAGATATCAACAATATATGACTATAC	2392
Db	2507	AATGTGATGAAATATGACAGACTTTGGACTGCGCCAGAGATATCAACAATATATGACTATAC	2566
QY	2393	AAAAAGACCAACCATATGGCGGCTTCCGATGAAGTATGATGCTCAGAGAGCCCTGTTGAT	2452
Db	2567	AAAAAGACCAACCAATGGCGGCTTCCGATGAAGTATGATGCTCAGAGAGCCCTGTTGAT	2626
QY	2453	AGAGATATCACTCATCAGATGATGATGTCTGTCTCTCGGGGTATTAATGTGGAGATCTTC	2512
Db	2627	AGAGATATCACTCATCAGATGATGATGTCTGTCTCTCGGGGTATTAATGTGGAGATCTTC	2686
QY	2513	ACTTTAGGGGCTCGCCCTTACCAGGGATTCCTCGTAGAGAACTTTTAAAGCTCTGAA	2572
Db	2687	ACTTTAGGGGCTCGCCCTTACCAGGGATTCCTCGTAGAGAACTTTTAAAGCTCTGAA	2746
QY	2573	GAAAGACACAGAAATGATTAAGCAGCCGACCACTGACCAACGAACGTACATGATGAG	2632
Db	2747	GAAAGACACAGAAATGATTAAGCAGCCGACCACTGACCAACGAACGTACATGATGAG	2806
QY	2633	GACTGTGGCATGCAGTGGCCTCCAGAGACCAAGTTCGAAGCAAGTTGTGAAAGACTTG	2692
Db	2807	GACTGTGGCATGCAGTGGCCTCCAGAGACCAAGTTCGAAGCAAGTTGTGAAAGACTTG	2866
QY	2693	GATCGAATTCATCTCTCAACCAATGAGAAATCTTGAGCCTCAGCCACACTCTGAA	2752
Db	2867	GATCGAATTCATCTCTCAACCAATGAGAAATCTTGAGCCTCAGCCACACTCTGAA	2926
QY	2753	CAGTATTCACCTAGTTTACCTCTGACCAAGAAAGTCTTGTCTTCCAGAGATGATCTGTT	2812
Db	2927	CAGTATTCACCTAGTTTACCTCTGACCAAGAAAGTCTTGTCTTCCAGAGATGATCTGTT	2986
QY	2813	TTTTCTCCAGACCCCATGCTCTTACGAAACCATGCTTCTCCAGTATCCACATAAAGGC	2872
Db	2987	TTTTCTCCAGACCCCATGCTCTTACGAAACCATGCTTCTCCAGTATCCACATAAAGGC	3046
QY	2873	AGGTGTTAAACATGATGACTGTGCTGCTGCTGCCCAACAGACACACACTGGGAACT	2932
Db	3047	AGGTGTTAAACATGATGACTGTGCTGCTGCTGCCCAACAGACACACACTGGGAACT	3106
QY	2933	AGCTACACTGAGCAGGAGACCATGCTCCAGAGCTTGTTGTCTCACTTGATATATG	2992
Db	3107	AGCTACACTGAGCAGGAGACCATGCTCCAGAGCTTGTTGTCTCACTTGATATATG	3166
QY	2993	GATCAGAGAGTAAATATTTGAAAAAGTAAATGAGATATGTGTAAGATTTATACAGTTG	3052
Db	3167	GATCAGAGAGTAAATATTTGAAAAAGTAAATGAGATATGTGTAAGATTTATACAGTTG	3226

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QY      3053  AAAACTGTATCTTCCCGAGAGAGAAGGTTCTGGAGCAGTGC 3106
Db      3227  AAAACTGTATCTTCCCGAGAGAGAAGGTTCTGGAGCAGTGC 3280

RESULT 4
US-11-019-829-39
; Sequence 39, Application US/11019829
; Publication No. US20050136465A1
; GENERAL INFORMATION:
; APPLICANT: Hoffmann-La Roche Inc.
; TITLE OF INVENTION: Novel targets for obesity from subcutaneous fat
; FILE REFERENCE: 22304
; CURRENT APPLICATION NUMBER: US/11/019,829
; CURRENT FILING DATE: 2004-12-22
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 39
; LENGTH: 4574
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: fibroblast growth factor receptor 2 transcript variant 2
; LOCATION: (1)..(4574)
; OTHER INFORMATION: LOCusID: 2263; NM_022366
US-11-019-829-39

Query Match      97.0%; Score 3013.2; DB 13; Length 4574;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 3097; Conservative 0; Mismatches 8; Indels 9; Gaps 7.

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Db 767 GAGGTGCGTGCCTGTTGAAAGATGCCGCGTGATCATGTTGACTAAGATGGGGTGCAAC 826
Qy 653 TTGGGGCCCAACATATGAGACATGCTTTATTTGGGAGTACTTGAAGATAAAGGGCCGCA 712
Db 827 TTGGGGCCCAACATATGAGACATGCTTTATTTGGGAGTACTTGAAGATAAAGGGCCGCA 886
Qy 713 CCTAGAGACTCCGGCCCTATGCTTATGTAAGTGAAGTGTGAAGTGTGAAGTGTGAAGTGTGA 772
Db 887 CCTAGAGACTCCGGCCCTATGCTTATGTAAGTGAAGTGTGAAGTGTGAAGTGTGAAGTGTGA 946
Qy 773 TACTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 832
Db 947 TACTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1006
Qy 833 GGTGCGGAAGATTTTGTGATGAGAAACATTAACAACAAGAGACCATTAAGTGAACCAAC 892
Db 1007 GGTGCGGAAGATTTTGTGATGAGAAACATTAACAACAAGAGACCATTAAGTGAACCAAC 1066
Qy 893 ACAGAAAAGATGGAAGAAAGCGGCTCCATGCTGTGCTGCGGCGCAACATGCAAGTTTCCG 952
Db 1067 ACAGAAAAGATGGAAGAAAGCGGCTCCATGCTGTGCTGCGGCGCAACATGCAAGTTTCCG 1126
Qy 953 TGCCACGCGGGGGGGAACCAATATGCAACCATGCGGTGCTGAAAAACGGGAGAGATT 1012
Db 1127 TGCCACGCGGGGGGGAACCAATATGCAACCATGCGGTGCTGAAAAACGGGAGAGATT 1186
Qy 1013 AAGCAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1072
Db 1187 AAGCAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1246
Qy 1073 GAAAGTGTGCTCCATCTGACAGAGGAAATTAACCTGTGTGATGAGAAATGAAATACGG 1132
Db 1247 GAAAGTGTGCTCCATCTGACAGAGGAAATTAACCTGTGTGATGAGAAATGAAATACGG 1306
Qy 1133 TCCATCAATCAACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1192
Db 1307 TCCATCAATCAACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1366
Qy 1193 CAAGCGGACTGCGGCAAAATGCTTCAACATGCTGCGAGAGACGTAAGATTGCTGCG 1252
Db 1367 CAAGCGGACTGCGGCAAAATGCTTCAACATGCTGCGAGAGACGTAAGATTGCTGCG 1426
Qy 1253 AAGTTTACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1312
Db 1427 AAGTTTACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1486
Qy 1313 AAGTAATACGAGGCGGCGGCTGCTTCAAGGTTCTCAAGCACTCGGGGATTAAT 1372
Db 1487 AAGTAATACGAGGCGGCGGCTGCTTCAAGGTTCTCAAGGTTCTCGGGGATTAAT 1546
Qy 1373 AGTTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1432
Db 1547 AGTTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1606
Qy 1433 ATATGTAAGTCTTCAATTAATATAGGCGAGGCAACATGCTGCGGCTCACTGCTGCG 1492
Db 1607 ATATGTAAGTCTTCAATTAATATAGGCGAGGCAACATGCTGCGGCTCACTGCTGCG 1666
Qy 1493 CCAAAAACAGCAAGCGCTGGAAGAGAAAGAGATTACAGCTTCCCAAGCTACCTGAG 1552
Db 1667 CCAAAAACAGCAAGCGCTGGAAGAGAAAGAGATTACAGCTTCCCAAGCTACCTGAG 1726
Qy 1553 ATAGCAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1612
Db 1727 ATAGCAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1786
Qy 1613 TGCCGATGAGAAACAGCAAG 1672
Db 1787 TGCCGATGAGAAACAGCAAG 1846
Qy 1673 CTGACCAAAAGTATCCCTGCGGAGAGACAGTAAACATTTCCGCTGAGTCACTCTCTCC 1732
Db 1847 CTGACCAAAAGTATCCCTGCGGAGAGACAGTAAACATTTCCGCTGAGTCACTCTCTCC 1906

Qy 1733 ATGAATCCCAACACCCGCTGATGAGATTAACAACAGGCTCTCTTCAACGGCAGACACC 1792
Db 1907 ATGAATCCCAACACCCGCTGATGAGATTAACAACAGGCTCTCTTCAACGGCAGACACC 1966
Qy 1793 CCCATGCTGAGAGGGGCTCCGAGTATGAATCTTCCAGAGAGACCAAAATGGAGTTTCCA 1852
Db 1967 CCCATGCTGAGAGGGGCTCCGAGTATGAATCTTCCAGAGAGACCAAAATGGAGTTTCCA 2026
Qy 1853 AAGATTAAGCTGACACTGAGGCAAGCCCTGGAGAGAGTTGCTTTGGGCAATGATGATGAT 1912
Db 2027 AAGATTAAGCTGACACTGAGGCAAGCCCTGGAGAGAGTTGCTTTGGGCAATGATGATGATGAT 2086
Qy 1913 GCGGAAGCAGTGGGAATGACAAAGACCAAGGCGGATCAAGCTGAGCGGCTGAAG 1972
Db 2087 GCGGAAGCAGTGGGAATGACAAAGACCAAGGCGGATCAAGCTGAGCGGCTGAAG 2146
Qy 1973 ATGTTGAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2032
Db 2147 ATGTTGAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2206
Qy 2033 ATGAAGAT 2092
Db 2207 ATGAAGAT 2266
Qy 2093 GGGGCTCTCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2152
Db 2267 GGGGCTCTCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2326
Qy 2153 GCCCGAGGCGCACCCGGGATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2212
Db 2327 GCCCGAGGCGCACCCGGGATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2386
Qy 2213 ATGACCTTCAAGGACTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2272
Db 2387 ATGACCTTCAAGGACTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2446
Qy 2273 GCTTCCCAAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2332
Db 2447 GCTTCCCAAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2506
Qy 2333 AATGAT 2392
Db 2507 AATGAT 2566
Qy 2393 AAAAAACCAACATGAGGCGGCTTCAAGTCAAGTGAATGCTTCAAGACCTCTGTTGAT 2452
Db 2567 AAAAAACCAACATGAGGCGGCTTCAAGTCAAGTGAATGCTTCAAGACCTCTGTTGAT 2626
Qy 2453 AAGATTAATCACTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACTCA 2512
Db 2627 AAGATTAATCACTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACTCA 2686
Qy 2513 ACTTTAGGGGGGCTGCGCTTCAACAGGATTCCTGGAGAGAACTTTTAACTGCTGAAG 2572
Db 2687 ACTTTAGGGGGGCTGCGCTTCAACAGGATTCCTGGAGAGAACTTTTAACTGCTGAAG 2746
Qy 2573 GAAAGCAACAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2632
Db 2747 GAAAGCAACAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2806
Qy 2633 GACTGTGGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2692
Db 2807 GACTGTGGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2866
Qy 2693 GATGCAATTTCACTCTCAACCAATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2752
Db 2867 GATGCAATTTCACTCTCAACCAATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2926
Qy 2753 CAGTATTCACCTAGTTACCTGACACAAGAGTTCTTGTCTTCAAGAGATGATGATGATGAT 2812
Db 2927 CAGTATTCACCTAGTTACCTGACACAAGAGTTCTTGTCTTCAAGAGATGATGATGATGATGAT 2986

OY	2813	TTTTCTCAGACCCCATGCTTTAGGAACATAGCTTCTCTCAGTATCCACAATATAAGGC	2872
Db	2987	TTTTCTTCAGACCCCATTGCGAACCAATGCTTCTCTCAGTATCCACAATATAAGGC	3046
OY	2873	AGTGTTAAAAATGATGATGACTGTGCTGCTGCTGCCAACAAGACATGGAACT	2932
Db	3047	AGTGTTAAAAATGATGATGACTGTGCTGCTGCTGCCAACAAGACATGGAACT	3106
OY	2993	AGCTTACATGAGCAGGAGAACATGCTCCCCAGAAGCTGTTGTCCTCACCTGTATATATG	2992
Db	3107	AGCTTACATGAGCAGGAGAACATGCTCCCCAGAAGCTGTTGTCCTCACCTGTATATATG	3166
OY	2993	GATCAGAGAGATTAATAATTGGAAAAAGTATCAGCANATGTGTAAAGATTATACAGTTG	3052
Db	3167	GATCAGAGAGATTAATAATTGGAAAAAGTATCAGCATGTGTGTAAAGATTATACAGTTG	3226
OY	3053	AAAACCTTGAATCTTCCCCCAGAGAGAAAGAAAGTTTCTGGAGCAGTAGACATGC	3106
Db	3227	AAAACCTTGAATCTTCCCCCAGAGAGAAAGAAAGTTTCTGGAGCAGTAGACATGC	3280

RESULT 5

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/ Sequence 132, Application US/11072175
/ Publication No. US2006002994A1
/ GENERAL INFORMATION:
/ APPLICANT: Bristol-Myers Squibb Company
/ TITLE OF INVENTION: IDENTIFICATION OF GENES FOR PREDICTING ACTIVITY OF COMPOUNDS THAT
/ TITLE OF INVENTION: INTERACT WITH AND/OR MODULATE PROTEIN TYROSINE KINASES AND/OR
/ TITLE OF INVENTION: PROTEIN TYROSINE KINASE PATHWAYS IN BREAST CELLS
/ FILE REFERENCE: D0273A CIP
/ CURRENT APPLICATION NUMBER: US/11/072,175
/ CURRENT FILING DATE: 2005-03-05
/ PRIOR APPLICATION NUMBER: US 60/406,385
/ PRIOR FILING DATE: 2002-08-27
/ PRIOR APPLICATION NUMBER: US 10/648,593
/ PRIOR FILING DATE: 2003-08-26
/ NUMBER OF SEQ ID NOS: 571
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 132
/ LENGTH: 4574
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ US-11-072-175-132

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Query Match 97.0%; Score 3013.2; DB 16; Length 4574;

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Best Local Similarity 99.5%; Pred. No. 0;
Matches 3097; Conservative 0; Mismatches 8; Indels 9; Gaps 7.
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QY	1	CCCGGAGCAAGTTTGGTGGAGGCAAGC-CAGAGCTGATCTTCTTCTCTGTTCC	59
Db	168	CTCGGAGCAAGTTTGGTGGAGGCAAGCCAAAGCTGATGTCCTTCTTCTCTGTTCC	227
QY	60	CCAAATCCGAGGGCAGCCCGCGGGCGTATG--GGCTCTCTCGCAAGCTGGGTTAAGC	116
Db	228	CCAAATCCCA-GCAGCCTCGCGAGCGTATGCTCCGCGCTCTCCGAGCTGGGGTATGC	286
QY	117	G-TGAAGCCCGGAGGCTTGGCGCGCGCAAGACCAGACCACTCTTCTGCGTTTGGAA	175
Db	287	GCTGAAGCCCGGAGGCTTGGCGCGCGCAAGCCCAAGACCACTCTTCTGCGTTTGGAA	346
QY	176	GTTTGCTCCCGCAACCCCGGGGCTCGTGCCTTTCTCATCTCCGACCAAGCCGGGGGC-CGGG	234
Db	347	GTTTGCTCCCGCAACCCCGGGGCTCGTGCCTTTCTCATCTCCGACCAAGCCGGGGGCGCGGG	406
QY	235	GACAAACAAGGTGCGGAGAGAGGTTGCATTCAATGACTCAGACAGCAGC-GCAGCGC	293
Db	407	GACAAACAAGGTGCGGAGAGAGGTTGCCATTCAATGACTCAGACAGCAGCGGACAGCGC	466
QY	294	CTCGGTTCTGAGCCCAACCGCA-GCTGAAGGCAATTGCGCGTAGTCCATATCCCGGTAGAGA	352
Db	467	CTCGGTTCTGAGCCCAACCGCAAGCTGAAGGCAATTGCGCGTAGTCCATATCCCGGTAGAGA	526

[illegible]

[illegible]

Db	1368	AAGCCGACATCGCCGCAAAATGCTCCACAGTGGTCGAGGAGACGTAGAGTTGTCTGCA	1427
QY	1254	AGGTTTACAGGATGCCCCAGCCCCACATCCAGTGGATCAAGCACTGTGGAAAAGAACGGCA	1313
Db	1428	AGGTTTACAGTGGATGCCCAAGCCCCACATCCAGTGGATCAAGCACTGTGGAAAAGAACGGCA	1487
QY	1314	GTAAATACGGGCCCCGACGGGCTGCTCACTCAAGTTCTTCAGCACTCGGGATTAATA	1373
Db	1488	GTAAATACGGGCCCCGACGGGCTGCTCACTCAAGTTCTTCAGCACTCGGGATTAATA	1547
QY	1374	GTTCCATGCAAGAGTGTGCTGTCTGT-----TCATGTGACCGAGCGGAGTCTGAGG	1427
Db	1548	CCAGGACCAAGAAATGAGGTTCTCTAATTTCCGAATGTAACTTTTGAGAGCGCTGGGG	1607
QY	1428	AATATATATGTAAGTGTCTCAATATATATAGGGCAGGCAACAGTGTGCTGCTCACTG	1487
Db	1608	AATATATGCTGTTGGCGGGTAAATCTTATTTGGGATATCTTTCACTGTGCATGTGTGACAG	1667
QY	1488	TCCTGCCAAAACAGCAAGCGGCTTGAGAGAAAAGAGATTAACGTTTCCCGACATACC	1547
Db	1668	TTCTGGC-----AGCGCTGGAAGAGAAAAGAGATTAACGTTTCCCGACATACC	1718
QY	1548	TGAGATATGCCATTTATCTGCATTAAGGGTCTCTTAATCGCCTGTATAGTGTGTACAGTCA	1607
Db	1719	TGAGATATGCCATTTATCTGCATTAAGGGTCTCTTAAATGCGCTGTATAGTGTGTACAGTCA	1778
QY	1608	TCCTGTGCCAATGAAAGAACAGCAACAGCAAGAGCAGACTTCAGCAGCAGCGGCTGTGC	1667
Db	1779	TCCTGTGCCAATGAAAGAACAGCAACAGCAAGAGCAGACTTCAGCAGCAGCGGCTGTGC	1838
QY	1668	ACAAGCTGACCAAAAGTATCCCTCTGCGGAGACAGTAAACGTTTCGGTGAATCTCACT	1727
Db	1839	ACAAGCTGACCAAAAGTATCCCTCTGCGGAGACAGTAAACGTTTCGGTGAATCTCACT	1898
QY	1728	CCTCATTAATCTTCAACACCCCCCTGTGTGAGAGATTAACAACGCGTCTTCAACGGCAG	1787
Db	1899	CCTCATTAATCTTCAACACCCCCCTGTGTGAGAGATTAACAACGCGTCTTCAACGGCAG	1958
QY	1788	ACAACCCCATGCTGGCAGGGGTCTCCGAGTGTGAACCTTCCAGAGGACCCAATAATGGAGT	1847
Db	1959	ACAACCCCATGCTGGCAGGGGTCTCCGAGTGTGAACCTTCCAGAGGACCCAATAATGGAGT	2018
QY	1848	TTCCAAAGATTAAGCTGACACTGTGGCAAGCCCTTGGAGAAAGTTGCTTTGGGCAAGTG	1907
Db	2019	TTCCAAAGATTAAGCTGACACTGTGGCAAGCCCTTGGAGAAAGTTGCTTTGGGCAAGTG	2078
QY	1908	TCATGGCCGAAGCAGTGGGAATTGACAAAGCAAGCCCAAGAGCGGTCAACCGTGGCG	1967
Db	2079	TCATGGCCGAAGCAGTGGGAATTGACAAAGCAAGCCCAAGAGCGGTCAACCGTGGCG	2138
QY	1968	TGAAGATGTGAAAGATGATGTGCAAGAGAAAGCCTTCTGATGTGCTGTCAGAGATGG	2027
Db	2139	TGAAGATGTGAAAGATGATGTGCAAGAGAAAGCCTTCTGATGTGCTGTCAGAGATGG	2198
QY	2028	AGATGATGAAGATGATTGGGAAACAAAGAAATATCATAAATCTTCTTGAAGCTTGACAC	2087
Db	2199	AGATGATGAAGATGATTGGGAAACAAAGAAATATCATAAATCTTCTTGAAGCTTGACAC	2258
QY	2088	AGGATGGGCTTCTTAATGTCATATGTTGAGTATGCTCTTAAAGGCAACTCCGAGAAATAC	2147
Db	2259	AGGATGGGCTTCTTAATGTCATATGTTGAGTATGCTCTTAAAGGCAACTCCGAGAAATAC	2318
QY	2148	TCGAGGCCGGAGGCAACCGGAGATGAGATCTCTATGACATTTAACGTTTCTTGAG	2207
Db	2319	TCGAGGCCGGAGGCAACCGGAGATGAGATCTCTATGACATTTAACGTTTCTTGAG	2377
QY	2208	AGCAGATGACTTCAAGACTTGTGTCAATGCACTTACCACTGCGCAGACGATGAGT	2267
Db	2379	AGCAGATGACTTCAAGACTTGTGTCAATGCACTTACCACTGCGCAGACGATGAGT	2438
QY	2268	ACTTGGCTTCCAAAATGATATTCATCGAGATTTAGCAGCCAGAAATGTTTGTGTACAG	2327

Db 2439 ACTGGCTTCCAAAATGATTCATCGAGATTAGACAGAAATGTTTGTATACAG 2498
Qy 2328 AAAACATGTGATGAAATATGACAGATCTTGGACTGCCGAGATATCAACATATGACT 2387
Db 2499 AAAACATGTGATGAAATATGACAGATCTTGGACTGCCGAGATATCAACATATGACT 2558
Qy 2388 ATTACAAAAGACCAACATGGGGCTTCCAGTCAAGTGAAGTGTCCAGAAAGCCCTGT 2447
Db 2559 ATTACAAAAGACCAACATGGGGCTTCCAGTCAAGTGAAGTGTCCAGAAAGCCCTGT 2618
Qy 2448 TTGATAGATATATCATCTCATCAGAGTATGTCTGTCTTCCGGGTGTATATGTGGAGA 2507
Db 2619 TTGATAGATATATCATCTCATCAGAGTATGTCTGTCTTCCGGGTGTATATGTGGAGA 2678
Qy 2508 TCTTCACTTTAGGGGGCTGCGCTTACCCAGGATTTCCCTGGAGAACTTTTAAGCTGC 2567
Db 2679 TCTTCACTTTAGGGGGCTGCGCTTACCCAGGATTTCCCTGGAGAACTTTTAAGCTGC 2738
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Qy 2628 TGAAGGAGATGTGGCATGACAGTCCCTCCAGAGACCAACGTTCAAGCAGTTGTAGAA 2687
Db 2799 TGAAGGAGATGTGGCATGACAGTCCCTCCAGAGACCAACGTTCAAGCAGTTGTAGAA 2858
Qy 2688 ACTTGATGATATCTCACTCTCAACCAATGAGAAATCTTGAACCTCAGCAACTC 2747
Db 2859 ACTTGATGATATCTCACTCTCAACCAATGAGAAATCTTGAACCTCAGCAACTC 2918
Qy 2748 TCGAAGATATCACTAGTACCTCGACACAAAGATCTTGTCTTCAAGAGATAT 2807
Db 2919 TCGAAGATATCACTAGTACCTCGACACAAAGATCTTGTCTTCAAGAGATAT 2978
Qy 2808 CTGTTTTTCTCCAGACCCCATGCTTACGAAACATGCTTCTCTCAGTATCCACATTA 2867
Db 2979 CTGTTTTTCTCCAGACCCCATGCTTACGAAACATGCTTCTCTCAGTATCCACATTA 3038
Qy 2868 ACGGAGTGTAAACATGATGATGTGTCTGCTGTCTCCCAACAGACAGCACTGG 2927
Db 3039 ACGGAGTGTAAACATGATGATGTGTCTGCTGTCTCCCAACAGACAGCACTGG 3098
Qy 2928 AACCTAGCTACACTGAGGAGAGACCAAGCCCTCCAGAGCTTGTCTCCACTGTAT 2987
Db 3099 AACCTAGCTACACTGAGGAGAGACCAAGCCCTCCAGAGCTTGTCTCCACTGTAT 3158
Qy 2988 ATATGATCAGAGAGATTAATATTTGAAAAAGTATCAGATATGTGTAAAGATTATAC 3047
Db 3159 ATATGATCAGAGAGATTAATATTTGAAAAAGTATCAGATATGTGTAAAGATTATAC 3218
Qy 3048 AGTTGAAACCTTGTAATCTTCCCGAGAGAGAAAGGTTTCTGAGACAGTGAATGC 3106
Db 3219 AGTTGAAACCTTGTAATCTTCCCGAGAGAGAAAGGTTTCTGAGACAGTGAATGC 3277

RESULT 7
US-11-019-829-42
; Sequence 42, Application US/11019829
; Publication No. US20050136465A1
; GENERAL INFORMATION:
; APPLICANT: Hoffmann-La Roche Inc.
; TITLE OF INVENTION: Novel targets for obesity from subcutaneous fat
; FILE REFERENCE: 22304
; CURRENT APPLICATION NUMBER: US/11/019,829
; CURRENT FILING DATE: 2004-12-22
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 42
; LENGTH: 4575
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: fibroblast growth factor receptor 2 transcript variant 5

; LOCATION: (1)..(4575)
; OTHER INFORMATION: LocusID: 2263; NM_022972
US-11-019-829-42
Query Match 91.7%; Score 2849.4; DB 13; Length 4575;
Best Local Similarity 96.5%; Pred. No. 0;
Matches 3020; Conservative 0; Mismatches 71; Indels 38; Gaps 9;
Qy 1 CCGCGAGCAAGTTTGTGTGAGGCAAG-CAAGCTGATGTCCTTCTCTGCTTCC 59
Db 168 CTGGGAGCAAGTTTGTGTGAGGCAAGCCCAAGCTGTGATCTTCTCTCTCTCTCC 227
Qy 60 CCAAAATCCGAGGGGAGCCCGCGGGGATATG--GCGCTCTCCGAGCTTGGATCCG 116
Db 228 CCAAAATCCGAGGGGAGCCCGCGGGGATATG--GCGCTCTCCGAGCTTGGATCCG 287
Qy 117 G-TGAAGCCCGGAGAGCTTGGCGCGCGGAGAACCCAGAACCACTCTTCTGCTTGA 175
Db 288 GCTGAAGCCCGGAGAGCTTGGCGCGCGGAGAACCCAGAACCACTCTTCTGCTTGA 347
Qy 176 GTTGTCTCCCGCAACCCCGGGGCTGCTGCTTCTCATATCCGACCCAGCGGGGCG-066 234
Db 348 GTTGTCTCCCGCAACCCCGGGGCTGCTGCTTCTCATATCCGACCCAGCGGGGCG-066 407
Qy 235 GACAAACAGATGCGGAGAGAGCTTGCATCAAGTGAATGAGAGAGAGAGAGAGAGAG 293
Db 408 GACAAACAGATGCGGAGAGAGCTTGCATCAAGTGAATGAGAGAGAGAGAGAGAGAG 467
Qy 294 CTGCGTCTGAGGCCCAACCGCA-GCTGAAGGATGCGGTATGATCCCGGTAGAGGA 352
Db 468 CTGCGTCTGAGGCCCAACCGCAAGGATGCGGTATGATCCCGGTATGAGAGGA 527
Qy 353 AGTGTGCAATGAGATTAACCTTCAACATGAGATATGAGAGAGAGAGAGAGAGAGAG 412
Db 528 AGTGTGCAATGAGATTAACCTTCAACATGAGATATGAGAGAGAGAGAGAGAGAGAG 587
Qy 413 GTAACCATGATGAGCTGGGGGCTGTTTCACTCTGCTGCTGCTGCTGCTGCTGCTG 472
Db 588 GTAACCATGATGAGCTGGGGGCTGTTTCACTCTGCTGCTGCTGCTGCTGCTGCTG 647
Qy 473 TCCCTGCGCGGCGCTCTTCAAGTTAGTTAGAGATACCAATAGAGCCAGAGAGCA 532
Db 648 TCCCTGCGCGGCGCTCTTCAAGTTAGTTAGAGATACCAATAGAGCCAGAGAGCA 707
Qy 533 CCAACCAATATCAAAATCTTCAACCAAGATGATGCTGCGGCAAGGAGAGAGAGAG 592
Db 708 CCAACCAATATCAAAATCTTCAACCAAGATGATGCTGCGGCAAGGAGAGAGAGAG 767
Qy 593 GAGGTGCGCTGCTGTTGAAGATGCGCGGATGATGATGATGATGATGATGATGATG 652
Db 768 GAGGTGCGCTGCTGTTGAAGATGCGCGGATGATGATGATGATGATGATGATGATG 827
Qy 653 TTGGGCGCCCAACATAGGACAGTGTATATGGGAGATCTTCAAGTAAAGGCGCCACA 712
Db 828 TTGGGCGCCCAACATAGGACAGTGTATATGGGAGATCTTCAAGTAAAGGCGCCACA 887
Qy 713 CCTAGAGATCCGGGCTCTTATGCTTGTATGCTGCAAGTATGATGATGATGATGATG 772
Db 888 CCTAGAGATCCGGGCTCTTATGCTTGTATGCTGCAAGTATGATGATGATGATGATG 947
Qy 773 TACTTCATGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 832
Db 948 TACTTCATGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1007
Qy 833 GGTGCGGAAGTTTGTGATGAGAGACATTAACCAAGAGAGAGAGAGAGAGAGAGAG 892
Db 1008 GGTGCGGAAGTTTGTGATGAGAGACATTAACCAAGAGAGAGAGAGAGAGAGAGAG 1067
Qy 893 ACAGAAAAGATGAAAAGAGGCTTCAAGTGTGCTGCGGCGCAACATCTCAAGTTTGGC 952
Db 1068 ACAGAAAAGATGAAAAGAGGCTTCAAGTGTGCTGCGGCGCAACATCTCAAGTTTGGC 1127
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Db 1128 TGCCAGCCGGGGGAAACCATGCGCAATGCGGTGCTGAAGAAAGGAGAGTTT 1187
OY 1013 AAGCAGGAGCATTCGATTGGAGGCTACAAAGGTAAGAAACAGCACTGAGGCTCATATG 1072
Db 1188 AAGCAGGAGCATTCGATTGGAGGCTACAAAGGTAAGAAACAGCACTGAGGCTCATATG 1247
OY 1073 GAAAGTGTGCTCCATCTTGAAGAGGAAATTAATCCTGTGTAGTGAAGATGAATCGGG 1132
Db 1248 GAAAGTGTGCTCCATCTTGAAGAGGAAATTAATCCTGTGTAGTGAAGATGAATCGGG 1307
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Db 1368 CAAGCCGAGCTGCGGCAAAATGCTCCACAGTGTGCGAGAGAGAGTGAAGTTGTCTGC 1427
OY 1253 AAGGTTTACAGTATGCGGAGCCCAATCCAGTGAATCAAGCAGTGAAGAAAGAGCGC 1312
Db 1428 AAGGTTTACAGTATGCGGAGCCCAATCCAGTGAATCAAGCAGTGAAGAAAGAGCGC 1487
OY 1313 AGTAATATCGGGCCGAGAGGCTGCCCTCAAGGTTCTCAAGGCTTCAAGGCGCGCC 1372
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OY 1373 AGTTCAAATGC-----AGAGTGTGCTGCTGTGTCAATGTGACGAGCG 1417
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OY 1478 TGGCTCACTGTCTCTCCAAAACAGAGAGGCTGGAAGAAAGAGATTAACAGTTCC 1537
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OY 1538 CCAGACTACTGAGATGAGCAATTAATCTGATAGGGGCTTCTTAATGCGCTGTATGAGT 1597
Db 1719 CCGAGACTACTGAGATGAGCAATTAATCTGATAGGGGCTTCTTAATGCGCTGTATGAGT 1778
OY 1598 GTAACAGTATCTGTGCGGAATGAAGAACAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 1657
Db 1779 GTAACAGTATCTGTGCGGAATGAAGAACAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 1838
OY 1658 CCGGCTGTGCAAGAGTGAAGCAAGTATCCCGCTGCGGAGACAGGTACAGTTCCGCT 1717
Db 1839 CCGGCTGTGCAAGAGTGAAGCAAGTATCCCGCTGCGGAGACAGGTACAGTTCCGCT 1892
OY 1718 GAGTCAAGTCTCTCCATGAATCTCAACACCCCGCTGTGAGATTAACAACAGCTCTCT 1777
Db 1893 GAGTCAAGTCTCTCCATGAATCTCAACACCCCGCTGTGAGATTAACAACAGCTCTCT 1952
OY 1778 TCAACGGCAGACACCCCAATGCTGCGAGGGGTCTCCGAGTATGAATCTTCAAGAGACCA 1837
Db 1953 TCAACGGCAGACACCCCAATGCTGCGAGGGGTCTCCGAGTATGAATCTTCAAGAGACCA 2012
OY 1838 AATATGGAATTTTCCAAAGATTAAGCTGAAGTGGGGAAGCCCTGAGGAAGAGTTGCTT 1897
Db 2013 AATATGGAATTTTCCAAAGATTAAGCTGAAGTGGGGAAGCCCTGAGGAAGAGTTGCTT 2072
OY 1898 GGGCAAGTGTATATGCGGAGAGAGTGGGAATTTGAAGAAAGCAAGCCCAAGAGAGCGCTC 1957
Db 2073 GGGCAAGTGTATATGCGGAGAGAGTGGGAATTTGAAGAAAGCAAGCCCAAGAGAGCGCTC 2132
OY 1958 ACCGTGCGCTGAAGATGTTGAAGATATGCAAGAGAAAGACCTTTCTGATCTGTG 2017
Db 2133 ACCGTGCGCTGAAGATGTTGAAGATATGCAAGAGAAAGACCTTTCTGATCTGTG 2192
OY 2018 TCAGATATGAGATATGAAGATGATTTGGGAAACAGAAATATCTTAATCTTCTTGA 2077

Db 2193 TCAGATATGAGATATGAAGATGATTTGGGAAACAGAAATATCTTAATCTTCTTGA 2252
OY 2078 GCTTGACACAGAGATGGGCTCTCTATGTCAATGTTGAATATGCTTTAAAGCACTC 2137
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OY 2138 CGAATAATCCCGAGGCGGAGGCGCACCGGGATGGAGTACTCTATGACATTTAACCGT 2197
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OY 2258 CGATGAGATATCTTGCTTCCCAAAATGTATATATGAGATTTAGAGCCAGAAAGTT 2317
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OY 2318 TTGGTTACAGAAACAAATGTATGAATAATAGCAGACTTGGACTCGCAGAGATATCAAC 2377
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Db 2553 AATATGACTATTTACAAAAGACCAACCAATGGCGGCTTCCAGTCAAAGTGGATGCTCA 2612
OY 2438 GAAAGCTGTTTGAATGATATACATCTCATAGATATGTCTGTCTCTGGGGTGTGA 2497
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OY 2498 ATGAGGAGAGATCTTCACTTAAGGGGGCGCGCCCTACCCAGAGGATTCGAGTGAAGAACTT 2557
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OY 2558 TTTAAGCTGCTGAAGAAAGACACAGAAATGATTAAGCAAGCAAGCAAGCAAGCAAGCTG 2617
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OY 2618 TACATGATGATGAGGAGCTGTGGCATGCAATGCCCTCCAGAACCAAGCTTCAAGAG 2677
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OY 2678 TTGGAAGAGACTTGGATGCAATCTCACTCTCAACCAATGAGAAATTAAGTGAAGCTC 2737
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OY 2738 AGCAACCTCTGCAACAGTATTAACCTAGTTACCTTGAACAAGAAAGTTCTTGTCTCA 2797
Db 2913 AGCAACCTCTGCAACAGTATTAACCTAGTTACCTTGAACAAGAAAGTTCTTGTCTCA 2972
OY 2798 GAGATGATTTCTGTTTTTCTCCAGACCCCATGCCCTTACCAACATGCCCTTCCAGTAT 2857
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Db 3033 CCACACATTAACGGCAGGTATTAACATGATGACTGTCTGCTGTCCCCAAGAGAGAG 3092
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OY 3098 AGATTTATACAGTTGAAGAACTTGTAACTTCCCGCAGAGAGAGAAAGTTTCTGAGACA 3097
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OY 3098 GTGAGCTGC 3106
Db 3273 GTGAGCTGC 3281

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RESULT 8
US-09-954-556-25
; Sequence 25, Application US/09954556
; Publication No. US20030078219A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Scott Cooper
; TITLE OF INVENTION: ANTISENSE MODULATION OF FIBROBLAST GROWTH FACTOR RECEPTOR 2 EXPRE
; FILE REFERENCE: RTS-0250
; CURRENT APPLICATION NUMBER: US/09/954,556
; CURRENT FILING DATE: 2001-09-14
; NUMBER OF SEQ ID NOS: 108
; SEQ ID NO 25
; LENGTH: 3080
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (612)..(3080)
US-09-954-556-25

Query Match      90.3%; Score 2806.2; DB 3; Length 3080;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 2879; Conservative 0; Mismatches 8; Indels 8; Gaps 6;

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DB      186 CTCGGAGGCAAGTTGTGTGAGGCAACGCAAGCTGAGTCTTCTCTCTCTCTCC 245
QY      60 CCAATTCGAGGCGAGCCCGCGGCGTCAATG---GGCTCTCTCGGAGCCTGGGTAACG 116
DB      246 CCAATTCGAGGCGAGCCCGCGGCGTCAATGCGCGGCTCTCTCGGAGCCTGGGTAACG 305
QY      117 G-TGAAGCCGAGGAGCTTGAGCGCGGCGGAGACCAAGAACCACTCTCTGCTTGA 175
DB      306 GCTGAGCCCGGAGGAGCTTGAGCGCGGCGGAGACCAAGAACCACTCTCTGCTTGA 365
QY      176 GTTGCTCCCGCAACCCCGGCGTCTGTGCTTCTCCATCCGACCCGCGGCGC-CGCG 234
DB      366 GTTGCTCCCGCAACCCCGGCGTCTGTGCTTCTCCATCCGACCCGCGGCGCGCGG 425
QY      235 GACCAACAGCGTGCAGGAGAGGCTTCAATCAATGACTGACAGACAC-CGACGCC 293
DB      426 GACCAACAGCGTGCAGGAGAGGCTTCAATCAATGACTGACAGACAGCGGCGACGCC 485
QY      294 CTCGGTCTGAGCCCAACCGCA-GCTGAGGCAATTGCGGTAAGTCCCGTGAAGGA 352
DB      486 CTCGGTCTGAGCCCAACCGCAAGCTGAGGCAATTGCGGTAAGTCCCGTGAAGGA 545
QY      353 AGTGTGCAAGTGGATTAACTGTCACATGAGATGAAAGAGACCGGGGATTTGTACC 412
DB      546 AGTGTGCAAGTGGATTAACTGTCACATGAGATGAAAGAGACCGGGGATTTGTACC 605
QY      413 GTAACCATGTCACTGCGGAGTCTTCAATCTGCTGTGTGTGTCACTGCAACTTGG 472
DB      606 GTAACCATGTCACTGCGGAGTCTTCAATCTGCTGTGTGTGTCACTGCAACTTGG 665
QY      473 TCCCTGAGCCCGGCGCTTCAAGTTAGTTAGGATACCACTTGAAGCAGAAAGGCA 532
DB      666 TCCCTGAGCCCGGCGCTTCAAGTTAGTTAGGATACCACTTGAAGCAGAAAGGCA 725
QY      533 CCAACCAATACCAATCTCTCAACCAAGATGTAGTGTGCGCAAGGAGTGTGCTA 592
DB      726 CCAACCAATACCAATCTCTCAACCAAGATGTAGTGTGCGCAAGGAGTGTGCTA 785
QY      593 GAGGTGCGTCTGTTGAAAGATGCGCGGTGATGATGTTGAGATTAAGATGGGTGAC 652
DB      786 GAGGTGCGTCTGTTGAAAGATGCGCGGTGATGATGTTGAGATTAAGATGGGTGAC 845
QY      653 TTGGGGCCCAACATAGACAGTGTATTGTGGGAGTACTTGCAGATTAAGGCGGCACA 712
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DB      846 TTGGGGCCCAACATAGACAGTGTATTGTGGGAGTACTTGCAGATTAAGGCGGCACG 905
QY      713 CCTAGAGACTCCGGCTCTATGTCTGTACTGCAAGTGAAGCTGTGACAGTGAACCTTG 772
DB      906 CCTAGAGACTCCGGCTCTATGTCTGTACTGCAAGTGAAGCTGTGACAGTGAACCTTG 965
QY      773 TACTTCATGTGAATGTCAAGATGCAATCTCATCCGGAGATGATGATGACCAACGAT 832
DB      966 TACTTCATGTGAATGTCAAGATGCAATCTCATCCGGAGATGATGATGACCAACGAT 1025
QY      833 GGTGCGAAGATTTTGTCAGTGAGAACAGTAAACAACAAGAGACCACTATGAGCAAC 892
DB      1026 GGTGCGAAGATTTTGTCAGTGAGAACAGTAAACAACAAGAGACCACTATGAGCAAC 1085
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DB      1086 ACAGAAAGATGAAAGAGCGGCTCCATGCTGTGCTGCGGCAACACTGTCAAGTTCCG 1145
QY      953 TGCCCAAGCCGGGGGGAACCAATGCAACCATGCGGTGCTGAAAAACGGGAAGGTT 1012
DB      1146 TGCCCAAGCCGGGGGGAACCAATGCAACCATGCGGTGCTGAAAAACGGGAAGGTT 1205
QY      1013 AAGCAGAGCATTCGATTTGAGGCTTAAAGTATACGAACCAAGCACTGAGCCTCATTTAG 1072
DB      1206 AAGCAGAGCATTCGATTTGAGGCTTAAAGTATACGAACCAAGCACTGAGCCTCATTTAG 1265
QY      1073 GAAAGTGTGTCATCTGACAAAGGAAATTATACCTGTGTATGAGATGATATCGGG 1132
DB      1266 GAAAGTGTGTCATCTGACAAAGGAAATTATACCTGTGTGTGAGATGATATCGGG 1325
QY      1133 TCCATCAATCAAGATACCACTGTGATGTGTGAGACCATTCGCTCAACGGGCTCATTC 1192
DB      1326 TCCATCAATCAAGATACCACTGTGATGTGTGAGACCATTCGCTCAACGGGCTCATTC 1385
QY      1193 CAAGCCGAGCTCCGGCAAAATGCTTCAAGTGTGCGAGAGACGTATAGTTGTCTCG 1252
DB      1386 CAAGCCGAGCTCCGGCAAAATGCTTCAAGTGTGCGAGAGACGTATAGTTGTCTCG 1445
QY      1253 AAGGTTTACATGATATGCCAGCCCAATCAAGTATGATCAAGCAGTGAAGAAAGCGC 1312
DB      1446 AAGGTTTACATGATATGCCAGCCCAATCAAGTATGATCAAGCAGTGAAGAAAGCGC 1505
QY      1313 AGTAAATACGGGCGCGAGCGGCTGCTTCAAGTGTCTCAAGCACTTCGGGATTAAT 1372
DB      1506 AGTAAATACGGGCGCGAGCGGCTGCTTCAAGTGTCTCAAGCACTTCGGGATTAAT 1565
QY      1373 AGTTCCAATGCAAGATGTGCTCTGTTCATATGACCGAGCGGATGCTTGCGGAATAT 1432
DB      1566 AGTTCCAATGCAAGATGTGCTCTGTTCATATGACCGAGCGGATGCTTGCGGAATAT 1625
QY      1433 ATATGTAAAGTCTCCAAATTAATATAGGAGCGCAACAGTCTGCTGCTCATCTGCTG 1492
DB      1626 ATATGTAAAGTCTCCAAATTAATATAGGAGCGCAACAGTCTGCTGCTCATCTGCTG 1685
QY      1493 CCAAAAACAGCAAGCGCTGGAAGAGAAAAAGAGATTAAGCTTCCCAAGACTACCTGAG 1552
DB      1686 CCAAAAACAGCAAGCGCTGGAAGAGAAAAAGAGATTAAGCTTCCCAAGACTACCTGAG 1745
QY      1553 ATAGCAATTTATGATAGGGGCTTCTTAACTGCTGATGATGATGATGATGATGATG 1612
DB      1746 ATAGCAATTTATGATAGGGGCTTCTTAACTGCTGATGATGATGATGATGATGATG 1805
QY      1613 TGCCGAATGAAAGACAGACCAAGAGCCAGACTTCAAGAGCCAGCCGCTGTGACAG 1672
DB      1806 TGCCGAATGAAAGACAGACCAAGAGCCAGACTTCAAGAGCCAGCCGCTGTGACAG 1865
QY      1673 CTGACCAACAGTATCCCTGCGGAGACAGATTAAGATTTGGGCTGATCCAGCTCTCC 1732
DB      1866 CTGACCAACAGTATCCCTGCGGAGACAGATTAAGATTTGGGCTGATCCAGCTCTCC 1925
QY      1733 ATGAATCTCAACACCCGCTGATGATTAACAACAGCTCTCTTCAACGGCAGACACC 1792
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Db 1926 ATGAACTCCAACACCCCGTGTGAGGATTAACAACGCTCTCTTCAACGGCAGACACC 1985
Qy 1793 CCATGCTGGAGGGGCTCTCGAGTATGAATCTTCAGAGGACCCAAATGGAGTTTCCA 1852
Db 1986 CCAATGCTGGAGGGGCTCTCGAGTATGAATCTTCAGAGGACCCAAATGGAGTTTCCA 2045
Qy 1853 AGAGATTAAGCTGACACTGGGCAAGCCCTGGAGAGAGTTGCTTGGGCAATGTGTCATG 1912
Db 2046 AGAGATTAAGCTGACACTGGGCAAGCCCTGGAGAGAGTTGCTTGGGCAATGTGTCATG 2105
Qy 1913 GCGGAAACAGTGGGAATTTGACAAAGACCAAGAGAGGGGCTTCACCGTGGCCGTGAAG 1972
Db 2106 GCGGAAACAGTGGGAATTTGACAAAGACCAAGAGAGGGGCTTCACCGTGGCCGTGAAG 2165
Qy 1973 ATGTTGAAAGATGATGTCACAGAGAAAGACCTTCTGATCTGTGTGTCAGAGATGAGATG 2032
Db 2166 ATGTTGAAAGATGATGTCACAGAGAAAGACCTTCTGATCTGTGTGTCAGAGATGAGATG 2225
Qy 2033 ATGAAGATGATTTGGGAAAACAAGAAATATCAATAATCTTCTTGGAGCCTGCAACAGAT 2092
Db 2226 ATGAAGATGATTTGGGAAAACAAGAAATATCAATAATCTTCTTGGAGCCTGCAACAGAT 2285
Qy 2093 GGGGCTCTATGTCATATGTTGATGATGCTCTAAGGCAACCTCCGGAATACCTCGGA 2152
Db 2286 GGGGCTCTATGTCATATGTTGATGATGCTCTAAGGCAACCTCCGGAATACCTCGGA 2345
Qy 2153 GCCCGAGGCGCACCCGGGATGAGTACTCTATGACATTAACCGTGTCTTGAAGAGCAG 2212
Db 2346 GCCCGAGGCGCACCCGGGATGAGTACTCTATGACATTAACCGTGTCTTGAAGAGCAG 2405
Qy 2213 ATGACCTTCAAGGACTTGTGTGTCATGCACTTACCGAGCTGGCGAGAGGATGAGTACTG 2465
Db 2273 GCTTCCCAAAATGATTCATCGAGATTAGAGTTCAGAGCAAAATGTTTGTATACGAAAC 2332
Qy 2466 GCTTCCCAAAATGATTCATCGAGATTAGAGTTCAGAGCAAAATGTTTGTATACGAAAC 2525
Db 2333 AATGATGATGAATATGACAGACTTTGCACTCCGCAAGATATCAACATATATGACTATTAC 2392
Qy 2526 AATGATGATGAATATGACAGACTTTGCACTCCGCAAGATATCAACATATATGACTATTAC 2585
Db 2393 AAAAAACCAACATGAGGCGGCTTCAGTCAAGTGAAGTCCCAAGACCCCTGTTGAT 2452
Qy 2586 AAAAAACCAACATGAGGCGGCTTCAGTCAAGTGAAGTCCCAAGACCCCTGTTGAT 2645
Db 2453 AGAGATTAACCTCATCAGAGTGAATCTGTGCTTCGAGGAGTTTAAATGGAGATCTTC 2512
Qy 2646 AGAGATTAACCTCATCAGAGTGAATCTGTGCTTCGAGGAGTTTAAATGGAGATCTTC 2705
Db 2513 ACTTTAGGGGGCTCGCCTTACCAGAGATTCCTCGTGAAGAACTTTTAAAGTGTGAAG 2572
Qy 2706 ACTTTAGGGGGCTCGCCTTACCAGAGATTCCTCGTGAAGAACTTTTAAAGTGTGAAG 2765
Db 2573 GAAAGCAACAGATGATGATGAGCAGCCTGCAACCAAGAACTTATCATGATGATGAG 2632
Qy 2766 GAAAGCAACAGATGATGATGAGCAGCCTGCAACCAAGAACTTATCATGATGATGAG 2825
Db 2633 GACTGTGGCAGTGAAGTGGCCCTCCAGAGACCAAGTTCAGACAGTGGTATGAAGACTTG 2692
Qy 2826 GACTGTGGCAGTGAAGTGGCCCTCCAGAGACCAAGTTCAGACAGTGGTATGAAGACTTG 2885
Db 2693 GATCGAATTTCTCACTCTCAACAACCAATGAGAAATCTTGAACCTGAGCCAACTCTCGAA 2752
Qy 2886 GATCGAATTTCTCACTCTCAACAACCAATGAGAAATCTTGAACCTGAGCCAACTCTCGAA 2945
Db 2753 CAGTATTAACCTTAAGTTCCTTGAACCAAGAAATTTCTTGTCTTCAAGAGATATTTCTGT 2812
Qy 2946 CAGTATTAACCTTAAGTTCCTTGAACCAAGAAATTTCTTGTCTTCAAGAGATATTTCTGT 3005
Db 2813 TTTTCTCCGAGACCCATGCTTAAAGAACCATGCTTCCATGATTCACATTAACGGC 2872
Qy 3006 TTTTCTCCGAGACCCATGCTTAAAGAACCATGCTTCCATGATTCACATTAACGGC 3065

Qy 2873 AGTGTAAAAATGCA 2887
Db 3066 AGTGTAAAAATGCA 3080

RESULT 9
US-09-954-456-293
; Sequence 293, Application US/09954456
; Patent No. US20020115057A1
; GENERAL INFORMATION:
; APPLICANT: Young, Paul
; TITLE OR INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Canc
; TITLE OR INVENTION: Sets
; FILE REFERENCE: 689290-76
; CURRENT APPLICATION NUMBER: US/09/954,456
; CURRENT FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: US/60/233,617
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US/60/234,052
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: US/60/234,923
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US/60/235,134
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US/60/235,637
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US/60/235,638
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US/60/235,711
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,720
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,840
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,863
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 2276
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 293
; LENGTH: 4268
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-954-456-293

Query Match 89.6%; Score 2781.8; DB 3; Length 4268;
Best Local Similarity 97.3%; Pred. No. 0;
Matches 2887; Conservative 0; Mismatches 62; Indels 18; Gaps 5;

Qy 149 CCCAAGACCACTTTCTGCGTTTGAAGTGTCTCCCGCAACCCCGGCTGTGCTTTC 208
Db 1 CCCAAGACCACTTTCTGCGTTTGAAGTGTCTCCCGCAACCCCGGCTGTGCTTTC 60

Qy 209 TCCATCCGACCCCAACGCGGGGC-CGGGCAACAACAGGTGCGAGAGAGCGTTGCCATTTC 267
Db 61 TCCATCCGACCCCAACGCGGGGC-CGGGCAACAACAGGTGCGAGAGAGCGTTGCCATTTC 120

Qy 268 AAGTACTGACAGCAGCAGC-CCAGCGCTCGGTTCTGAGCCGCAACGCA-GCTGAAGCA 325
Db 121 AAGTACTGACAGCAGCAGCAGCGCTCGGTTCTGAGCCGCAACGCAAGGCA 180

Qy 326 TTGGCGGTAATGTCATGCCCGTGAAGAGATGTCAGATGAGATTAAAGTTCACATGAGA 385
Db 181 TTGGCGGTAATGTCATGCCCGTGAAGAGATGTCAGATGAGATTAAAGTTCACATGAGA 240

Qy 386 TATGAAGAGACCGGGGATTTGTAACCTTAACATGTGTCAGCTGGGTTGTTTCACTGCG 445
Db 241 TATGAAGAGACCGGGGATTTGTAACCTTAACATGTGTCAGCTGGGTTGTTTCACTGCG 300

Qy 446 CTGTCGTGTGTCACCATGGAACCTTGTCTGCGCCGCGCTCTCTTCAAGTTAGTTAG 505
Db 301 CTGTCGTGTGTCACCATGGAACCTTGTCTGCGCCGCGCTCTCTTCAAGTTAGTTAG 360

506 GATACCACTTAGAGCCAGAGGCCAACCAATATCAATCTCTCAACAGAGAGT 565
561 GATACCACTTAGAGCCAGAGGCCAACCAATATCAATCTCTCAACAGAGAGT 420
566 TACGTGGCTGCGCCAGGGAGTCTGTAGAGTGGCTGTGTGAAGAGTCCGCGT 625
421 TACGTGGCTGCGCCAGGGAGTCTGTAGAGTGGCTGTGTGAAGAGTCCGCGT 480
626 ATCACTTGAAGCTAAGAGTGGGTGCACTTGGGGCCCAATATGACAGTCTTATGG 685
481 ATCACTTGAAGCTAAGAGTGGGTGCACTTGGGGCCCAATATGACAGTCTTATGG 540
686 GAGTACTTGCAGATTAAGGGCGCACTAGAGTCCGGCTCTATGCTGTACTGCC 745
541 GAGTACTTGCAGATTAAGGGCGCACTAGAGTCCGGCTCTATGCTGTACTGCC 600
746 AGTAGAGCTGTAGACAGTAACTTGGTACTTCACTGTGATGTCACAGATCCATCTCA 805
601 AGTAGAGCTGTAGACAGTAACTTGGTACTTCACTGTGATGTCACAGATCCATCTCA 660
806 TCCGAGATGATGAGAGTACACCCAGTGTGCGGAAGATTTGTGCTAGAGAACAGTAA 865
661 TCCGAGATGATGAGAGTACACCCAGTGTGCGGAAGATTTGTGCTAGAGAACAGTAA 720
866 AACAGAGAGCCATCTGAGCCACACAGAAAGATGAAAGGCGCTCATGCTGTG 925
721 AACAGAGAGCCATCTGAGCCACACAGAAAGATGAAAGGCGCTCATGCTGTG 780
926 CCTGCGGCAACACTGTCAAGTTTGGCTCCGAGCGGGGGAGCCCAATGCGAACATG 985
781 CCTGCGGCAACACTGTCAAGTTTGGCTCCGAGCGGGGGAGCCCAATGCGAACATG 840
986 CGGTGGCTGAAAAACGGGAAGATTAAAGCAGAGCATGCACTTGAAGGCTTCAAGGTA 1045
841 CGGTGGCTGAAAAACGGGAAGATTAAAGCAGAGCATGCACTTGAAGGCTTCAAGGTA 900
1046 CGAAACCAACACTGAGGCTCATTTAGAAAGTGTGCTCCATCTGCAAGGGAAATTA 1105
901 CGAAACCAACACTGAGGCTCATTTAGAAAGTGTGCTCCATCTGCAAGGGAAATTA 960
1106 ACCGTGTAGTGAAGATGAATACGGGTCCATCAATCAACAGTACCACTGTGATTTG 1165
961 ACCGTGTAGTGAAGATGAATACGGGTCCATCAATCAACAGTACCACTGTGATTTG 1020
1166 GAGCGATGCTTCAACCGGCCCATCTTCAAGCGGACTGCGGCAATGCTTCAAGT 1225
1021 GAGCGATGCTTCAACCGGCCCATCTTCAAGCGGACTGCGGCAATGCTTCAAGT 1080
1226 GTTCGAGAGAGCTAAGTTTGTCTGCAAGTTTAAGTATGCCAGGCCCAATCCAG 1285
1081 GTTCGAGAGAGCTAAGTTTGTCTGCAAGTTTAAAGTATGCCAGGCCCAATCCAG 1140
1286 TGGATCAAGCAGTGAAGAAAGACGGCAGTAAATTAAGGGCGGCTGCTCACTC 1345
1141 TGGATCAAGCAGTGAAGAAAGACGGCAGTAAATTAAGGGCGGCTGCTCACTC 1200
1346 AAGGTTCTCAAGCAGTGGGGATTAATGTTCCATGCAAGAGTGTGCTGTGT----- 1400
1201 AAGGTTCTCAAGGCGCGGTGTTAAACCAACGGAACAAAGATGAGGTTCTCTATAT 1260
1401 -TCAATGTACCGAGCGGATGTGTGGGAATATATATGTAAGTCTCCAAATATATAGG 1459
1261 CGGAATGTAACTTTAAGAGCGTGGGAAATATACGTGCTTGGCGGTAATTTATTTGG 1320
1460 CAGGCAACAGTCTGCTGCTGCTCACTGTCTGCAAAACAGCAACGCGCTGAGAGAA 1519
1321 ATATCTTTTCACTGTGATGTTGAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1371
1520 AAGAGATTAACAGCTTCTCCAGACTACCTGAGATAGCAATTTATCTGATAGGGGTCT 1579
1372 AAGAGATTAACAGCTTCTCCAGACTACCTGAGATAGCAATTTATCTGATAGGGGTCT 1431
1580 TTATATGCTGTATGTGTGTAACAGTATCTGTGTGCAATGAAGAACAGCAAGAAAG 1639

1432 TTATATGCTGTATGTGTGTAACAGTATCTGTGTGCAATGAAGAACAGCAAGAAAG 1491
1640 CCAAGCTTCAAGAGCAACCGGCTGTGCAAAAGTGAACCAACATATCCCTGGGGAGA 1699
1492 CCAAGCTTCAAGAGCAACCGGCTGTGCAAAAGTGAACCAACATATCCCTGGGGAGA 1551
1700 CAGGTAAAGTTTGGCTGAGTCAAGTCTTCAATGAATCCCAACACCGCTGTGTAG 1759
1552 CAGGTAAAGTTTGGCTGAGTCAAGTCTTCAATGAATCCCAACACCGCTGTGTAG 1611
1760 ATTAACAACCGCTCTTCAACCGCAGACACCCCATGCTGGCAGGGGTCTTCCAGTAT 1819
1612 ATTAACAACCGCTCTTCAACCGCAGACACCCCATGCTGGCAGGGGTCTTCCAGTAT 1671
1820 GAATTTCCAGAGAGCCCAAAATGGAGTTTCCAAAGATTAAGCTGACCTGGGCAAGCC 1879
1672 GAATTTCCAGAGAGCCCAAAATGGAGTTTCCAAAGATTAAGCTGACCTGGGCAAGCC 1731
1880 CTGGAGAAAGTTTGGCTTGGGCAAGTGTGATGCGGAAAGCAGTGGAAATTTGACAAAGAC 1939
1732 CTGGAGAAAGTTTGGCTTGGGCAAGTGTGATGCGGAAAGCAGTGGAAATTTGACAAAGAC 1791
1940 AAGCCCAAGAGAGCGGTCAACCGTGGCGTGAAGATGTTGAAGATGATGCCACAGAGAA 1999
1792 AAGCCCAAGAGAGCGGTCAACCGTGGCGTGAAGATGTTGAAGATGATGCCACAGAGAA 1851
2000 GACTTTCTGATCTGTGTGATGAGATGATGAGATGATGAGATGATGAGATGATGAGAT 2059
1852 GACTTTCTGATCTGTGTGATGAGATGATGAGATGATGAGATGATGAGATGATGAGAT 1911
2060 ATCATTAATCTTCTGAGGCTGCAACAGATGAGGCTCTCTATGTCTAGTGTAGTAT 2119
1912 ATCATTAATCTTCTGAGGCTGCAACAGATGAGGCTCTCTATGTCTAGTGTAGTAT 1971
2120 GCTCTTAAAGGCACTTCCAGATACTCCAGAGCCCGGAGCCACCCGGAGTGAAGTAC 2179
1972 GCTCTTAAAGGCACTTCCAGATACTCCAGAGCCCGGAGCCACCCGGAGTGAAGTAC 2031
2180 TCTTATGATTAACCGGTCTCTGAGAGCAGATGATCTTCAAGACTTGTGTATATC 2239
2032 TCTTATGATTAACCGGTCTCTGAGAGCAGATGATCTTCAAGACTTGTGTATATC 2091
2240 ACTTACCGAGTGGCCAGAGGATGAGTACTTGGGCTTCCCAAAATGATTAATCAAGAT 2299
2092 ACTTACCGAGTGGCCAGAGGATGAGTACTTGGGCTTCCCAAAATGATTAATCAAGAT 2151
2300 TTAGCAGCCAGAAATGTTTGTGAACAGAAACAAATGTATGATAATGACAGCTTTGA 2359
2152 TTAGCAGCCAGAAATGTTTGTGAACAGAAACAAATGTATGATAATGACAGCTTTGA 2211
2360 CTGCGCAGAGATTAACAAATATTAATTAACAAAGACCAATGGGGGCTTTCA 2419
2212 CTGCGCAGAGATTAACAAATATTAATTAACAAAGACCAATGGGGGCTTTCA 2271
2420 GTCAAGTGAATGCTTCCAGAAACCGCTTGTGAATGATTAACATCAAGTATGATC 2479
2272 GTCAAGTGAATGCTTCCAGAAACCGCTTGTGAATGATTAACATCAAGTATGATC 2231
2480 TGGTCTTGGGGGTGTAATGTGAGATCTTCACTTAAAGGGGCTGCGCTTACCAAGG 2539
2332 TGGTCTTGGGGGTGTAATGTGAGATCTTCACTTAAAGGGGCTGCGCTTACCAAGG 2391
2540 ATTCCGATGAGAACTTTTAAAGTCTGAAAGAGAGCAAGATGATTAAGCCAGCC 2599
2392 ATTCCGATGAGAACTTTTAAAGTCTGAAAGAGAGCAAGATGATTAAGCCAGCC 2451
2600 AACTGACCAAGAGTGAACATGATGATGAGAGAGCTGTGAGATGATGATGATGATGAT 2659
2452 AACTGACCAAGAGTGAACATGATGATGAGAGAGCTGTGAGATGATGATGATGATGAT 2511
2660 AACTGACCAAGAGTGAACATGATGATGAGAGAGCTGTGAGATGATGATGATGATGAT 2719

1021 GAGCAGTGCCTCACCGGCCCTCTCCAGCCGAGCTGCGGCAAAATGCTCCACAGTG 1080
1226 GTGCGAGGAGACGTAGATTGTCTGCAAGTTTACAGTATGCCAGCCGACATCCAG 1285
1081 GTGCGAGGAGACGTAGATTGTCTGCAAGTTTACAGTATGCCAGCCGACATCCAG 1140
1286 TGGATCAGACAGTGGAAAAAGACGACATTAATACGGGCCGAGAGGGGTGCTTACTTC 1345
1141 TGGATCAGACAGTGGAAAAAGACGACATTAATACGGGCCGAGAGGGGTGCTTACTTC 1200
1346 AAGGTTCCAAACACTCGGGGGAATAATGTTCCAAATGAGAGAGTGCTGCTGT----- 1400
1201 AAGGTTCTCAAGCCGCGCGGTGTACACACGACAAAGAGATGAGGTTCTTAATAT 1260
1401 -TCAATGTGACCGAGCGGAGTCTGCGGAATAATATATGTAAGTCTCCAAATTAATAGG 1459
1261 CGGAATGTAACTTTGAGGACGCTGGGGAAATAACGTCTGGCGGATTAATCTAATGGG 1320
1460 CAGGCCAACAGTCTGCTGCTGCTCACTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1519
1321 AATATCTTTCATCTGACATGTTGACATGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1371
1520 AAGGATTTACAGCTTCCGACATACCTGAGATGATGACATTTACATGAGGCTTCTC 1579
1372 AAGGATTTACAGCTTCCGACATACCTGAGATGATGACATTTACATGAGGCTTCTC 1431
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1552 CAGGTAACAGTTTGGCTGAGTCAAGCTCTCCATGATGATGATGATGATGATGATGATGAT 1611
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1672 GAACTTCCAGAGACCCCAAAATGGAGTTTCCAGATGATGATGATGATGATGATGATGATGAT 1731
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1732 CTGGGAGAGGTTGCTTGGGGAAGTGTCAATGCGGAGACAGTGGGAATTGACAAAGAC 1791
1940 AAGCCCAAGAGAGGCTGACCGTGTGCGGAGATGTTGAAAGATGATGATGATGATGATGATGAT 1999
1792 AAGCCCAAGAGAGGCTGACCGTGTGCGGAGATGTTGAAAGATGATGATGATGATGATGATGAT 1851
2000 GAACTTCTGATCTGTGTCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2059
1852 GAACTTCTGATCTGTGTCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1911
2060 AATCATTAATCTTCTGAGCTGACACAGATGAGGCTCTCATGTCAATGATGATGAT 2119
1912 AATCATTAATCTTCTGAGCTGACACAGATGAGGCTCTCATGTCAATGATGATGAT 1971
2120 GCTCTAAAGCAACCTCCGAGATACCTCCGAGCCGAGAGGCAACCGGAGTGAAGTAC 2179
1972 GCTCTAAAGCAACCTCCGAGATACCTCCGAGCCGAGAGGCAACCGGAGTGAAGTAC 2031
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2240 AACTACAGCTGCGCAGAGGATGAGTCTTGGCTTCCCAAAATGATGATGATGATGATGATGAT 2299

2092 AACTACAGCTGCGCAGAGGATGAGTCTTGGCTTCCCAAAATGATGATGATGATGATGATGAT 2151
2300 TTAGAGCCAGAAATGTTTGGTAAACAGAAAACAATGATGAAATGAGACATTTGGA 2359
2152 TTAGAGCCAGAAATGTTTGGTAAACAGAAAACAATGATGAAATGAGACATTTGGA 2211
2360 CTGCGCAGAGATATCAACATATAGACTATTAACAAAAGACCAACCATGAGGCGCTTCCA 2419
2212 CTGCGCAGAGATATCAACATATAGACTATTAACAAAAGACCAACCATGAGGCGCTTCCA 2271
2420 GTCAATGATGATGCTCCAGAAAGCCCTGTTGATGATGATGATGATGATGATGATGATGATGAT 2479
2272 GTCAATGATGATGCTCCAGAAAGCCCTGTTGATGATGATGATGATGATGATGATGATGATGAT 2331
2480 TGTCTCTTGGGGGTATTAATGAGAGATCTTCACTTAAGGGGGGTGCGCCCTACCGAGG 2539
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2452 AACTGACACCAAGAACTGTACATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2511
2660 AAGCCAAAGTTCAAGACATGTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 2719
2512 AAGCCAAAGTTCAAGACATGTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 2571
2720 GAGGAATACCTTGACCTGAGCCAACTCTGCAACAGTATGATGATGATGATGATGATGATGATGAT 2779
2572 GAGGAATACCTTGACCTGAGCCAACTCTGCAACAGTATGATGATGATGATGATGATGATGATGAT 2631
2780 AAGAGTTCTTGTCTTCAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2839
2632 AAGAGTTCTTGTCTTCAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2691
2840 CCAATGCTTCTCAGTATCCACATTAACGCACTGTTAAACATGATGATGATGATGATGATGAT 2899
2692 CCAATGCTTCTCAGTATCCACATTAACGCACTGTTAAACATGATGATGATGATGATGATGAT 2751
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2752 GCTGTCCCAAAACGAGACAGACCTGAGACCTGATGATGATGATGATGATGATGATGATGATGAT 2811
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2812 TCCAGAGCTTGTGTCTCCACTTGTATATGATGATGATGATGATGATGATGATGATGATGATGAT 2871
3020 TTAATGACATATGTTTAAAGATTTATACATGTTGAAAATTGTAATCTTCCGAGAGAG 3079
2872 TTAATGACATATGTTTAAAGATTTATACATGTTGAAAATTGTAATCTTCCGAGAGAG 2931
3080 AAGAGGTTTCTGAGAGAGTGAAGTGC 3106
2932 AAGAGGTTTCTGAGAGAGTGAAGTGC 2956

RESULT 11
US-09-954-556-3
Sequence 3, Application US/09954556
Publication No. US20030078219A1
GENERAL INFORMATION:
APPLICANT: Brett P. Monia
APPLICANT: Susan M. Freiler
APPLICANT: Scott Cooper
TITLE OR INVENTION: ANTISENSE MODULATION OF FIBROBLAST GROWTH FACTOR RECEPTOR 2 EXPRES-
S
CURRENT APPLICATION NUMBER: US/09/954,556
CURRENT FILING DATE: 2001-09-14
NUMBER OF SEQ ID NOS: 108
SEQ ID NO 3

LENGTH: 4268
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (274) ... (2739)
us-09-954-556-3

Query Match 89.6%; Score 2781.8; DB 3; Length 4268;
Best Local Similarity 97.3%; Pred. No. 0;
Matches 2887; Conservative 0; Mismatches 62; Indels 18; Gaps 5;

QY 149 CCAAGAGCACTCTTCTGCTTTGGAGTTGCTCCCGCAACCCCGGCTGTGCTTTC 208
DB 1 CCAAGAGCACTCTTCTGCTTTGGAGTTGCTCCCGCAACCCCGGCTGTGCTTTC 60
QY 209 TCCATCCCGAGCCCAACCGGGGCG-CCGGGACAAACACAGGTCCGGAGGAGCGGTGCATTC 267
DB 61 TCCATCCCGAGCCCAACCGGGGCGCGGGACAAACAGGTCCGGAGGAGCGGTGCATTC 120
QY 268 AAGTACTGCAGACAGCAGC-GCAGCGCTCGGTTCTAGGCCCAACCGA-GCTGAAGCA 325
DB 121 AAGTACTGCAGACAGCAGCAGCGGAGCGCTCGGTTCTAGGCCCAACCGAGGCTGAAGCA 180
QY 326 TTGGCGGTAGTCCATGCTCCGTAGAGAAAGTGTGCAGATGGGATTAACTCCATGAGGA 385
DB 181 TTGGCGGTAGTCCATGCTCCGTAGAGAAAGTGTGCAGATGGGATTAACTCCATGAGGA 240
QY 386 TATGGAAGAAGACCGGGGATTGTATCCGTAAACCATGTGAGTGGGGTGGTTTCACTGC 445
DB 241 TATGGAAGAAGACCGGGGATTGTATCCGTAAACCATGTGAGTGGGGTGGTTTCACTGC 300
QY 446 CTGGTCTGTGTACCATGGCAACTTGTCCCTGGCCCGGCTCTCTTCAATTAGTTAG 505
DB 301 CTGGTCTGTGTACCATGGCAACTTGTCCCTGGCCCGGCTCTCTTCAATTAGTTAG 360
QY 506 GATACCACTTAAAGACCCAGAGAGCCCAACCAATTCCTTCAACCAAGAGT 565
DB 361 GATACCACTTAAAGACCCAGAGAGCCCAACCAATTCCTTCAACCAAGAGT 420
QY 566 TACGTGGTGGCCCGGAGAGTCCGTAGAGTGGCGCTGCTGTAAAGAGTCCGGCGG 625
DB 421 TACGTGGTGGCCCGGAGAGTCCGTAGAGTGGCGCTGCTGTAAAGAGTCCGGCGG 480
QY 626 ATCAGTTGGACTAAGATGGGCTGTGCACTTGGGCCCCCAACATAGGACAGTGTAT 685
DB 481 ATCAGTTGGACTAAGATGGGCTGTGCACTTGGGCCCCCAACATAGGACAGTGTAT 540
QY 686 GAGTACTTGCAGATTAAGGGCCGACACTTAAAGACTCCGGCTCTATGCTTTACTGCC 745
DB 541 GAGTACTTGCAGATTAAGGGCCGACACTTAAAGACTCCGGCTCTATGCTTTACTGCC 600
QY 746 AGTAGACGTGTAGACAGTGAACCTTGATCTTCAATGTGATGTGACAGATGCCATCTCA 805
DB 601 AGTAGACGTGTAGACAGTGAACCTTGATCTTCAATGTGATGTGACAGATGCCATCTCA 660
QY 806 TCCGAGATGATGAGGATGACACCGATGTGTGGAAATTTTGTCACTGAGAAACAGTAAC 865
DB 661 TCCGAGATGATGAGGATGACACCGATGTGTGGAAATTTTGTCACTGAGAAACAGTAAC 720
QY 866 AACAGAGAGCACCATATCTGACCAACACAGAAAGATGAAAGGCGCTCCATGCTG 925
DB 721 AACAGAGAGCACCATATCTGACCAACACAGAAAGATGAAAGGCGCTCCATGCTG 780
QY 926 CCTGGCGGCAACACTGTCAAGTTTGGCTGCCAGCGGGGGGAAACCAATGCAACCATG 985
DB 781 CCTGGCGGCAACACTGTCAAGTTTGGCTGCCAGCGGGGGGAAACCAATGCAACCATG 840
QY 986 CCGTGGCTGAAAAACGGGAAGAGTTTAAAGCAGAGCATGCAATTGAGGCTTACAAGGTA 1045
DB 841 CCGTGGCTGAAAAACGGGAAGAGTTTAAAGCAGAGCATGCAATTGAGGCTTACAAGGTA 900
QY 1046 CGAAACAGACACTGAGCCTCATTTATGAAAGTGTGCTCCATCTGACAAAGGAAATTAT 1105

DB 901 CGAAACAGACACTGAGCCTCATTTATGAAAGTGTGCTCCCATCTGACAAAGGAAATTAT 960
QY 1106 ACCGTGTAGTGAAGAAATGAATACGGGTCCATCAATCACAGTACCATGATGTTGG 1165
DB 961 ACCGTGTAGTGAAGAAATGAATACGGGTCCATCAATCACAGTACCATGATGTTGG 1020
QY 1166 GAGCGATCGCTCACCGGCCCCATCTCCAAAGCCGGAATGCGCGGAATGCTCCACAGTG 1225
DB 1021 GAGCGATCGCTCACCGGCCCCATCTCCAAAGCCGGAATGCGCGGAATGCTCCACAGTG 1080
QY 1226 GTGGAAGAGACGTAGAGTTTGTCTGCAAGTTTACAGTATGCGGACCCCATTCAG 1285
DB 1081 GTGGAAGAGACGTAGAGTTTGTCTGCAAGTTTACAGTATGCGGACCCCATTCAG 1140
QY 1286 TGATCAAGCAGTGAAGAAAGACGCAATTAACGGGCCCGACGGGCTGCTTACTC 1345
DB 1141 TGATCAAGCAGTGAAGAAAGACGCAATTAACGGGCCCGACGGGCTGCTTACTC 1200
QY 1346 AAGGTTCTCAAGCACTGGGGGATTAATAGTTCCATGACAGAGTCTGGGCTGT----- 1400
DB 1201 AAGGTTCTCAAGCGCGCGGCTGTTAACACCGACAAAGAGATTGAGTTCTTAATAT 1260
QY 1401 -TCAATGTGACCGAGCGGATGCTGGGAAATATATATGTAAGTCTCCAAATTATAGG 1459
DB 1261 CGGATGTAACTTTTGAGAGCGCTGGGGAATATACGTGCTGGGGGTAATTTATTTGG 1320
QY 1460 CAGGCCAACAGTCTGCTGCTCACTGCTCTGCCAAAACAGCAAGCGCTGGAAGAA 1519
DB 1321 ATATCTTTCACTCTGATAGTTGACAGTTCTGCC-----AGCGCTGGGAAGAA 1371
QY 1520 AAGGATTAACGTTCCCACTACCTGAGATAGCAATTTACTGATAGGGGCTTC 1579
DB 1372 AAGGATTAACGTTCCCACTACCTGAGATAGCAATTTACTGATAGGGGCTTC 1431
QY 1580 TTAATCGCTGTATGATGATTAACAGTCACTGTGCGGAATGAAGAACACGACCAAGAG 1639
DB 1432 TTAATCGCTGTATGATGATTAACAGTCACTGTGCGGAATGAAGAACACGACCAAGAG 1491
QY 1640 CCAGACTTCAGCAGCCAGCCGGCTGTGTGCAAACTGACCAAGCTTACCAAGCTATCCCTCGGAGA 1699
DB 1492 CCAGACTTCAGCAGCCAGCCGGCTGTGTGCAAACTGACCAAGCTTACCAAGCTATCCCTCGGAGA 1551
QY 1700 CAGGTAACAGTTTGGGCTGATCCAGCTCTCCATGAACTTCCAAACCCCGCTGTAGG 1759
DB 1552 CAGGTAACAGTTTGGGCTGATCCAGCTCTCCATGAACTTCCAAACCCCGCTGTAGG 1611
QY 1760 ATTAACAACCGCTCTCTTCAACGGCAGACACCCCATGCTGGCAAGGGTCTCCGATAT 1819
DB 1612 ATTAACAACCGCTCTCTTCAACGGCAGACACCCCATGCTGGCAAGGGTCTCCGATAT 1671
QY 1820 GAATCTTCAGAGACCCAAAATGGAGATTTTCCAAAGATAGTCAACCCCGCTGTAGG 1879
DB 1672 GAATCTTCAGAGACCCAAAATGGAGATTTTCCAAAGATAGTCAACCCCGCTGTAGG 1731
QY 1880 CTGGGAAGAGTTGCTTGGGCAAGTGTCTAATGGCGAAGCAGTGGGAATTGAACAAGAC 1939
DB 1732 CTGGGAAGAGTTGCTTGGGCAAGTGTCTAATGGCGAAGCAGTGGGAATTGAACAAGAC 1791
QY 1940 AAGCCCAAGAGCGGTCACCGTGGCCGTGAAGATGTTGAAGATGATGCCACAGAGAA 1999
DB 1792 AAGCCCAAGAGCGGTCACCGTGGCCGTGAAGATGTTGAAGATGATGCCACAGAGAA 1851
QY 2000 GACCTTTCTGATCTGTGTCAAGATGGAATGATGAAGATTTGGGAAACACAAGAT 2059
DB 1852 GACCTTTCTGATCTGTGTCAAGATGGAATGATGAAGATTTGGGAAACACAAGAT 1911
QY 2060 ATCATTAATCTTTTGGAGCTGTGCAACAGATGGGCTCTATGTCATGATGATAT 2119
DB 1912 ATCATTAATCTTTTGGAGCTGTGCAACAGATGGGCTCTCTATGTCATGATGATAT 1971
QY 2120 GCCTTAAGGCACTCCGAGATTACTCCGAGCCCGGAGGCCAACCAGGATGAGTAC 2179

Db 1972 GCCTTAAAGCACTCCAGATATCTCCGAGCCCGAGGACCCCGGATGAGTAC 2031
 Qy 2180 TCCATGACATTAACCGTGTCTTGAGAGCAGATGACTTCAAGACCTTGCTGATGC 2239
 Db 2032 TCCATGACATTAACCGTGTCTTGAGAGCAGATGACTTCAAGACCTTGCTGATGC 2091
 Qy 2240 ACCTACAGCTGCGCAGAGGATGAGTACTTGCGCTTCCAAAATGATCATCGAGT 2299
 Db 2092 ACCTACAGCTGCGCAGAGGATGAGTACTTGCGCTTCCAAAATGATCATCGAGT 2151
 Qy 2300 TTAGCAGCAGAAATGTTTGTATACAGAAAATATGTATGAAAATAGCAGACTTGG 2359
 Db 2152 TTAGCAGCAGAAATGTTTGTATACAGAAAATATGTATGAAAATAGCAGACTTGG 2211
 Qy 2360 CTGCGCAGAGATTCACAAATATGACTATTTACAAAAGACCAATGCGGCTTCCA 2419
 Db 2212 CTGCGCAGAGATTCACAAATATGACTATTTACAAAAGACCAATGCGGCTTCCA 2271
 Qy 2420 GTCAAGTGAATGCTCCAGAAAGCCCTGTGATGATGATACCTCATCAGATGATGC 2479
 Db 2272 GTCAAGTGAATGCTCCAGAAAGCCCTGTGATGATGATACCTCATCAGATGATGC 2331
 Qy 2480 TGGTCTTGGGGGTGTTATATGTTGAGAGATCTTCACTTATAGGGGCTGCGCTACCAAG 2539
 Db 2332 TGGTCTTGGGGGTGTTATATGTTGAGAGATCTTCACTTATAGGGGCTGCGCTACCAAG 2391
 Qy 2540 ATTCCGTTGAGAGAACTTTTAACTGCTGTAAGAAAGACAGAAATGATTAAGCAACC 2599
 Db 2392 ATTCCGTTGAGAGAACTTTTAACTGCTGTAAGAAAGACAGAAATGATTAAGCAACC 2451
 Qy 2600 AACTGACCAACCAAGATGATGATGATGATGATGATGATGATGATGATGATGATG 2659
 Db 2452 AACTGACCAACCAAGATGATGATGATGATGATGATGATGATGATGATGATGATG 2511
 Qy 2660 AGACCAACCTTCAAGCAGTGTAGAAAGCTTGAATGAAATCTCACTCTCAACCAAT 2719
 Db 2512 AGACCAACCTTCAAGCAGTGTAGAAAGCTTGAATGAAATCTCACTCTCAACCAAT 2571
 Qy 2720 GAGGAATACCTTGAACCTGAGCCAACTCTGAAACATGATCAGCTTACCTTGACAC 2779
 Db 2572 GAGGAATACCTTGAACCTGAGCCAACTCTGAAACATGATCAGCTTACCTTGACAC 2631
 Qy 2780 AGAAGTCTTGTCTTCAAGAGATGATGATGATGATGATGATGATGATGATGATG 2839
 Db 2632 AGAAGTCTTGTCTTCAAGAGATGATGATGATGATGATGATGATGATGATGATG 2691
 Qy 2840 CCATGCTTCTCTAGATTCACATTAACGAGATGTTAAACATGATGATGATGATG 2899
 Db 2692 CCATGCTTCTCTAGATTCACATTAACGAGATGTTAAACATGATGATGATGATG 2751
 Qy 2900 GCCTGTCCCAACAGGACAGACCTGAGAACTTATGCTACCTGAGCAGGAGACATGCC 2959
 Db 2752 GCCTGTCCCAACAGGACAGACCTGAGAACTTATGCTACCTGAGCAGGAGACATGCC 2811
 Qy 2960 TCCCAAGCTTGTGTCTTCACTTGTATATATGATGATGATGATGATGATGATG 3019
 Db 2812 TCCCAAGCTTGTGTCTTCACTTGTATATATGATGATGATGATGATGATGATG 2871
 Qy 3020 TAATCAGCATATGTTAAAGATTTATCAGTTGAAAATGTTATCTTCCCGAGAGAG 3079
 Db 2872 TAATCAGCATATGTTAAAGATTTATCAGTTGAAAATGTTATCTTCCCGAGAGAG 2931
 Qy 3080 AAGAAAGTTTCTGAGAGAGTGAAGTGC 3106
 Db 2932 AAGAAAGTTTCTGAGAGAGTGAAGTGC 2958

RESULT 12

US-09-968-007A-461
 ; Sequence 461, Application US/09968007A
 ; Publication No. US20040115625A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ebner, Reinhard

; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Sign
 ; FILE OF INVENTION: Gene Sets
 ; FILE REFERENCE: 689290-71
 ; CURRENT APPLICATION NUMBER: US/09/968, 007A
 ; PRIOR FILING DATE: 2001-10-02
 ; PRIOR APPLICATION NUMBER: US/60/237, 172
 ; PRIOR FILING DATE: 2000-10-02
 ; PRIOR APPLICATION NUMBER: US/60/237, 173
 ; PRIOR FILING DATE: 2000-10-02
 ; PRIOR APPLICATION NUMBER: US/60/237, 278
 ; PRIOR FILING DATE: 2000-10-02
 ; PRIOR APPLICATION NUMBER: US/60/237, 294
 ; PRIOR FILING DATE: 2000-10-02
 ; PRIOR APPLICATION NUMBER: US/60/237, 295
 ; PRIOR FILING DATE: 2000-10-02
 ; PRIOR APPLICATION NUMBER: US/60/237, 316
 ; PRIOR FILING DATE: 2000-10-02
 ; NUMBER OF SEQ ID NOS: 1001
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 461
 ; LENGTH: 4268
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-968-007A-461

Query Match 89.6%; Score 2781.8; DB 3; Length 4268;
 Best Local Similarity 97.3%; Pred. No. 0;
 Matches 2887; Conservative 0; Mismatches 62; Indels 18; Gaps 5;

Qy 149 CCCAAGAGACCACTTCTGCGTTGAGTGTGCTCCCGCAACCCGCGCTCGTCTTC 208
 Db 1 CCCAAGAGACCACTTCTGCGTTGAGTGTGCTCCCGCAACCCGCGCTCGTCTTC 60
 Qy 209 TCCATCCGACCCACGCGGGGCG-CCGAGCAACACAGTCTGCGAGAGAGCTTCCATTC 267
 Db 61 TCCATCCGACCCACGCGGGGCGCGGGGCAACACAGTCTGCGAGAGAGCTTCCATTC 120
 Qy 268 AAGTACCTGACACAGCAGC-AGAAGGCTCGGTTCTTGAGCCCAACCGA-AGTGAAGGA 325
 Db 121 AAGTACCTGACACAGCAGCAGCGGCTCGGTTCTTGAGCCCAACCGA-AGTGAAGGA 180
 Qy 326 TTGCGGTAGTCAATGCGCGGTAGAGAGTGTGAGATGAGATGAGATGAGATGAG 385
 Db 181 TTGCGGTAGTCAATGCGCGGTAGAGAGTGTGAGATGAGATGAGATGAGATGAG 240
 Qy 386 TATGAAAGAGACCGGGGATGTAACCTGATGATGATGATGATGATGATGATGATG 445
 Db 241 TATGAAAGAGACCGGGGATGTAACCTGATGATGATGATGATGATGATGATGATG 300
 Qy 446 CTGCTGTGTGATCAATGAGCACTTGTCCCTGCGCCCGGCTCTTCACTTATGATG 505
 Db 301 CTGCTGTGTGATCAATGAGCACTTGTCCCTGCGCCCGGCTCTTCACTTATGATG 360
 Qy 506 GATACCACTTATGAGCAGAGAGCAACCAACCAATATCAATCTCTCAACAGAGTG 565
 Db 361 GATACCACTTATGAGCAGAGAGCAACCAACCAATATCAATCTCTCAACAGAGTG 420
 Qy 566 TACGTGTGCTGCGCAGGGGAGTCTGATGATGATGATGATGATGATGATGATG 625
 Db 421 TACGTGTGCTGCGCAGGGGAGTCTGATGATGATGATGATGATGATGATGATG 480
 Qy 626 ATCAGTTGATCAATGATGATGATGATGATGATGATGATGATGATGATGATG 685
 Db 481 ATCAGTTGATCAATGATGATGATGATGATGATGATGATGATGATGATGATG 540
 Qy 686 GAGTACTTGCAGATTAAGGGGCGCAACCTAGAGACTCGGCGCTCTATGCTTGTATG 745
 Db 541 GAGTACTTGCAGATTAAGGGGCGCAACCTAGAGACTCGGCGCTCTATGCTTGTATG 600
 Qy 746 AGTACGCTGTAGACAGTGAACCTTGTATCTTCACTGATGATGATGATGATGATG 805
 Db 601 AGTACGCTGTAGACAGTGAACCTTGTATCTTCACTGATGATGATGATGATGATG 660

QY	806	TCCGAGATGATGAGAGTGAACCGAGTGTGCGGAAGATTTTGTCACTGAGAACAGTAAC	865
Db	661	TCCGAGATGATGAGAGTGAACCGAGTGTGCGGAAGATTTTGTCACTGAGAACAGTAAC	720
QY	866	AACAAGAGAGACCACTATCGAACCAACAACAAAAGATGAAAAGCGGCTCAATGCTGTG	925
Db	721	AACAAGAGAGACCACTATCGAACCAACAACAAAAGATGAAAAGCGGCTCAATGCTGTG	780
QY	926	CCTGCGGCAACACTGTCAAGTTTGCGTGCCAGCCGGGGGAAACCAATGCCAACATG	985
Db	781	CCTGCGGCAACACTGTCAAGTTTGCGTGCCAGCCGGGGGAAACCAATGCCAACATG	840
QY	986	CGGTGCTGAAAAACGGGAGAGGTTTAAGCAGAGCATGCGATTGAGGGCTACAGATA	1045
Db	841	CGGTGCTGAAAAACGGGAGAGGTTTAAGCAGAGCATGCGATTGAGGGCTACAGATA	900
QY	1046	CGAAACCAAGCACTGGAGCCTCATTAATGAAAGTGTGCTCCATCTGCAAGGGGAAATTAT	1105
Db	901	CGAAACCAAGCACTGGAGCCTCATTAATGAAAGTGTGCTCCATCTGCAAGGGGAAATTAT	960
QY	1106	ACCTGTAGTGGAGAAATGAATACGGGTCCATCAATCAACAGTACCACTGGATGTTGTG	1165
Db	961	ACCTGTGTGTGGAGAAATGAATACGGGTCCATCAATCAACAGTACCACTGGATGTTGTG	1020
QY	1166	GAGCGATGCTCACCGGCCCATCTCTCAAGCCGGACGTGCCGCAATGCTTCCACATGT	1225
Db	1021	GAGCGATGCTCACCGGCCCATCTCTCAAGCCGGACGTGCCGCAATGCTTCCACATGT	1080
QY	1226	GTTCGAGAGAGACGTAGAGTTTGTCTGCAAGGTTTCACTGATATGCCAGGCCCAATCAG	1285
Db	1081	GTTCGAGAGAGAGTAGAGTTTGTCTGCAAGGTTTCACTGATATGCCAGGCCCAATCAG	1140
QY	1286	TGGATCAAGCAGTGGAAAAAGAACCGGCAGTAAATACGGGCCCGAACGGCTGCTTCACTC	1345
Db	1141	TGGATCAAGCAGTGGAAAAAGAACCGGCAGTAAATACGGGCCCGAACGGCTGCTTCACTC	1200
QY	1346	AAGTTTCTCAAGCACTCGGGATTAATATGTTCAATGCAATAGTCTGTCTGT-----	1400
Db	1201	AAGTTTCTCAAGCGCGCGGTGTTAAACAACGGAACAAAGATTGAAGTTTCTTAATAT	1260
QY	1401	-TCAATGTGACCGAAGCCGATGTCTGGGGAATATATATGTAAGTGTCCAAATTATATGAG	1459
Db	1261	CGGAATGTAACTTTTGAAGACGCTGGGGAATATATGCTCTTGGCGGTATTTCTATGTGG	1320
QY	1460	CAGGCAACCACTGTGCTGCTGAGCTCACTGTCTGCCAAAACAGCAAGCCCTGGAAGAA	1519
Db	1321	ATATCTTTTCACTCTGCAATGTTGACAGTTTCTGCC-----AGCCCTGGAAGAA	1371
QY	1520	AAGAGATTACAGCTTCCCAAGACTACCTGAGATAGCATTTACTGATATAGGGGTCTTC	1579
Db	1372	AAGGAGATTACAGCTTCCCAAGACTACCTGAGATAGCATTTACTGATATAGGGGTCTTC	1431
QY	1580	TTAATGTGCTGTATGTGTGTAAACATCATCTGTGTGCCGAATGAAAGAACAGACCAAGAG	1639
Db	1432	TTAATGTGCTGTATGTGTGTAAACATCATCTGTGTGCCGAATGAAAGAACAGACCAAGAG	1491
QY	1640	CCAGACTTCAGAGACGACGCGCTGTGCAACAGTGAACCAACGTATCCCTGTGGAGGA	1699
Db	1492	CCAGACTTCAGAGACGACGCGCTGTGCAACAGTGAACCAACGTATCCCTGTGGAGGA	1551
QY	1700	CAGTAAACAGTTTCGGCTGAGTTCACAGCTCTTCATGAATCTCAACACCCCGTGTGTAGG	1759
Db	1552	CAGTAAACAGTTTCGGCTGAGTTCACAGCTCTTCATGAATCTCAACACCCCGTGTGTAGG	1611
QY	1760	ATPAACAACGCTCTCTTTCACACGGCAGACACCCCAATGCTGGCAGGGGTCTCCAGATAT	1819
Db	1612	ATPAACAACGCTCTCTTTCACACGGCAGACACCCCAATGCTGGCAGGGGTCTCCAGATAT	1671
QY	1820	GAACTTCCAGAGGACCAAAATGGGAGTTTCCAAAGATATACCTGACACTGGGCAAGCC	1879
Db	1672	GAACTTCCAGAGGACCAAAATGGGAGTTTCCAAAGATATACCTGACACTGGGCAAGCC	1731
QY	1880	CTGGGAGAGGTGTCTTTGGGCAAGTGTCAATGGCGAAGCATGGGGAATTGACAAAGAC	1939

Db	1732	CTGGGAAGAAGTTCCTTTGGGCAAGTGGTCAATGGCCGGAAGCAGTGGAAATTGACAAAGAC	1791
Qy	1940	AAGCCCAAGGAGGGCGGTCAACCGTGGCCGTGAAGATGTTGAAAGATGATGCCACAGAGAA	1999
Db	1792	AAGCCCAAGGAGGGCGGTCAACCGTGGCCGTGAAGATGTTGAAAGATGATGCCACAGAGAA	1851
Qy	2000	GACCTTTCGTACTGTGTGCAGAGATGAGATGATGAAATGATTTGGGAAACACAGAT	2059
Db	1852	GACCTTTCGTACTGTGTGCAGAGATGAGATGATGAAATGATTTGGGAAACACAGAT	1911
Qy	2060	ATCATTAATCTTCTTGGAGCTTGACACAGATGGGCTCTCATATGTCATATGTGAGAT	2119
Db	1912	ATCATTAATCTTCTTGGAGCTTGACACAGATGGGCTCTCATATGTCATATGTGAGAT	1971
Qy	2120	GGCCTTAAGGCAACTCCGAGATPACTCCGAGCCCGAGGCGCACCCGGGATGAGTAC	2179
Db	1972	GGCCTTAAGGCAACTCCGAGATPACTCCGAGCCCGAGGCGCACCCGGGATGAGTAC	2031
Qy	2180	TCCATGACATTAACCGTGTCTCTGAGAGCAGATGACCTTCAAGGACTTGTGTATGC	2239
Db	2032	TCCATGACATTAACCGTGTCTCTGAGAGCAGATGACCTTCAAGGACTTGTGTATGC	2091
Qy	2240	ACCTAACGCTGGCCAGACGAGATGATCTTGGCTTCCCAAAATGATTCATCGAGAT	2299
Db	2092	ACCTAACGCTGGCCAGACGAGATGATCTTGGCTTCCCAAAATGATTCATCGAGAT	2151
Qy	2300	TTAGCAGCAGAAATGTTTGGTATACAGAAACATGTGATGAATAATGACAGCTTTGGA	2359
Db	2152	TTAGCAGCAGAAATGTTTGGTATACAGAAACATGTGATGAATAATGACAGCTTTGGA	2211
Qy	2360	CTCGCAGAGATATCAACATATATAGCTATTTACAAAAGACCAACATGGCGCTTCCA	2419
Db	2212	CTCGCAGAGATATCAACATATATAGCTATTTACAAAAGACCAACATGGCGCTTCCA	2271
Qy	2420	GTCAAGTGGATGGCTCCAGAAAGCCCTGTTGATGATGATACATCATCAGATGATGTC	2479
Db	2272	GTCAAGTGGATGGCTCCAGAAAGCCCTGTTGATGATGATACATCATCAGATGATGTC	2331
Qy	2480	TGGTCTTCGGGGGTGTTAATGAGGAGATCTTCACTTTAAGGGGCTGCCCTAACCCAGG	2539
Db	2332	TGGTCTTCGGGGGTGTTAATGAGGAGATCTTCACTTTAAGGGGCTGCCCTAACCCAGG	2391
Qy	2540	ATTCCCGTGGAGGAATTTTTAAGCTGCTGAAGGAGGACACAGATGATTAAGCCAGCC	2599
Db	2392	ATTCCCGTGGAGGAATTTTTAAGCTGCTGAAGGAGGACACAGATGATTAAGCCAGCC	2451
Qy	2600	AACTGACCAACGAACTGTACATGATGATGAGGACTGTGGCATGCACTGCCCTCCAG	2659
Db	2452	AACTGACCAACGAACTGTACATGATGATGAGGACTGTGGCATGCACTGCCCTCCAG	2511
Qy	2660	AGACCAAGTTCACACAGCTGGTGTGAACATTTGATGCAATTTCTCACCTGACACACAT	2719
Db	2512	AGACCAAGTTCACACAGCTGGTGTGAACATTTGATGCAATTTCTCACCTGACACACAT	2571
Qy	2720	GAGGAATACTTGGACCTCAGCCAACTCTCGAACAGTATTCACCTAAGTTACCCTGACA	2779
Db	2572	GAGGAATACTTGGACCTCAGCCAACTCTCGAACAGTATTCACCTAAGTTACCCTGACA	2631
Qy	2780	AGAAATTCTGTTCTTTCAGAGATGATTTCTGTTTTTCTCCAGACCCCATGCTTAAGAA	2839
Db	2632	AGAAATTCTGTTCTTTCAGAGATGATTTCTGTTTTTCTCCAGACCCCATGCTTAAGAA	2691
Qy	2840	CCATGCTTCCTCAATATTCACACATTAACGGCAGTGTAAACATGATGATGCTGTCT	2899
Db	2692	CCATGCTTCCTCAATATTCACACATTAACGGCAGTGTAAACATGATGATGCTGTCT	2751
Qy	2900	GGCTGTCCCAACAGAGCAGCAGCTGGGAACTTAAGTCACTGACAGGAGACCATGCTC	2959
Db	2752	GGCTGTCCCAACAGAGCAGCAGCTGGGAACTTAAGTCACTGACAGGAGACCATGCTC	2811
Qy	2960	TCCAGAGGTTGTGTCTTCACTTGTATATATGATCAGAGAGTAAATATTGGAAAG	3019

Db 2812 TCCAGAGCTGTGTGTCTCCTCACTGTATATATGATCAGAGGATTAATTAATGGAAG 2871
QY 3020 TAATCAGCATATGTGTAAAGATTATTAACAGTTGAAACTTTGATTTTCCCGAGAGAG 3079
Db 2872 TAATCAGCATATGTGTAAAGATTATTAACAGTTGAAACTTTGATTTTCCCGAGAGAG 2931
QY 3080 AAGAGAGTTCTGAGACAGTGCATGCG 3106
Db 2932 AAGAGAGTTCTGAGACAGTGCATGCG 2958

RESULT 13
US-10-843-641A-3320
Sequence 3320, Application US/10843641A
Publication No. US20050064454A1
GENERAL INFORMATION:
APPLICANT: Avalon Pharmaceuticals, Inc.
TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using
TITLE OF INVENTION: Signature Gene Sets
FILE REFERENCE: 689290-189
CURRENT APPLICATION NUMBER: US/10/843,641A
CURRENT FILING DATE: 2004-05-12
PRIOR APPLICATION NUMBER: US/09/873,367
PRIOR FILING DATE: 2001-06-05
PRIOR APPLICATION NUMBER: US/09/954,531
PRIOR FILING DATE: 2001-09-18
PRIOR APPLICATION NUMBER: US/09/954,456
PRIOR FILING DATE: 2001-09-25
PRIOR APPLICATION NUMBER: US/09/962,436
PRIOR FILING DATE: 2001-09-25
PRIOR APPLICATION NUMBER: US/09/962,832
PRIOR FILING DATE: 2001-09-25
PRIOR APPLICATION NUMBER: US/09/964,824
PRIOR FILING DATE: 2001-09-27
PRIOR APPLICATION NUMBER: US/09/967,768
PRIOR FILING DATE: 2001-09-28
PRIOR APPLICATION NUMBER: US/09/968,007
PRIOR FILING DATE: 2001-10-02
PRIOR APPLICATION NUMBER: US/09/969,347
PRIOR FILING DATE: 2001-10-02
PRIOR APPLICATION NUMBER: US/09/969,708
PRIOR FILING DATE: 2001-10-03
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 8447
SOFTWARE: PatentIn version 3.0
SEQ ID NO 3320
LENGTH: 4268
TYPE: DNA
ORGANISM: Homo sapiens
US-10-843-641A-3320

Query Match 89.6%; Score 2781.8; DB 10; Length 4268;
Best Local Similarity 97.3%; Pred. No. 0;
Matches 2887; Conservative 0; Mismatches 62; Indels 18; Gaps 5;

QY 149 CCCAAGACCACTCTTGTGCTTGAAGTTGCTCCCGGACCCCGGGCTCGTCCGTTTC 208
Db 1 CCCAAGACCACTCTTGTGCTTGAAGTTGCTCCCGGACCCCGGGCTCGTCCGTTTC 60
QY 209 TCCATCCGACCCGAGCGGGGGC-CGGGGAACAACAAGTGCAGAGAGGTTGCCATTTC 267
Db 61 TCCATCCGACCCGAGCGGGGGC-CGGGGAACAACAAGTGCAGAGAGGTTGCCATTTC 120
QY 268 AAGTGAAGTGAAGAGC-GCAGCGCTCGGTTCTGAGCCGCA-GCTGAAGGA 325
Db 121 AAGTGAAGTGAAGAGC-GCAGCGCTCGGTTCTGAGCCGCA-GCTGAAGGA 180
QY 326 TTGCGGTGATCATGCTCCGTAGAGAGAGTGTCAATGAGATTAACTTCCACATGAGA 385
Db 181 TTGCGGTGATCATGCTCCGTAGAGAGAGTGTCAATGAGATTAACTTCCACATGAGA 240
QY 386 TATGAAGAGGACGGGAGATGTGTACCGTAAACATGATGAGTGGGATTCATCTGC 445

Db 241 TATGGAAGAGACCGGGAGTTGTGTACCGTAACATGTGACGTGGGCTGTTTCATCTGC 300
QY 446 CTGGTGTGTGACCATATGGCAACTTGTCCCTGGCGGGCCCTCTTCAAGTTAGTAG 505
Db 301 CTGGTGTGTGACCATATGGCAACTTGTCCCTGGCGGGCCCTCTTCAAGTTAGTAG 360
QY 506 GATACCAATTAAGAGCCAGAAAGAGCCAAACCAATATCAAAATCTTCAACAGAAATG 565
Db 361 GATACCAATTAAGAGCCAGAAAGAGCCAAACCAATATCAAAATCTTCAACAGAAATG 420
QY 566 TACGTGTGTGCGCCAGGGAGTGTCTAGAGGTGTGCTGCTGTGTAAGATGCCCTGT 625
Db 421 TACGTGTGTGCGCCAGGGAGTGTCTAGAGGTGTGCTGCTGTGTAAGATGCCCTGT 480
QY 626 ATCAATTTGAATTAAGATGAGGTGTGACTTTGGGGCCCAATAGACAGTGTATTAGG 685
Db 481 ATCAATTTGAATTAAGATGAGGTGTGACTTTGGGGCCCAATAGACAGTGTATTAGG 540
QY 686 GAGTACTTGCAGATTAAGGGGCGCCACACTAGAGACTCCGGCTCTATGTTGATCTGC 745
Db 541 GAGTACTTGCAGATTAAGGGGCGCCACACTAGAGACTCCGGCTCTATGTTGATCTGC 600
QY 746 AATAGACTGTAGACAGTGAACCTTGTATCTTCAATGTGAATGTCAAGATGCCATCTCA 805
Db 601 AATAGACTGTAGACAGTGAACCTTGTATCTTCAATGTGAATGTCAAGATGCCATCTCA 660
QY 806 TTCCGAGATGATGAGATGACACCGATGTGTGGGAAGTTTGTGATGAGAAAGCTAAC 865
Db 661 TTCCGAGATGATGAGATGACACCGATGTGTGGGAAGTTTGTGATGAGAAAGCTAAC 720
QY 866 AACAGAGAGCACATATGAGCAACAGAAAGATGAAAGCGGCTCATGCTGTG 925
Db 721 AACAGAGAGCACATATGAGCAACAGAAAGATGAAAGCGGCTCATGCTGTG 780
QY 926 CCTGGGCGCAACCTGTCAAGTTTGTGCTGCCAGCGGGGGAGAACCAATGCCAATG 985
Db 781 CCTGGGCGCAACCTGTCAAGTTTGTGCTGCCAGCGGGGGAGAACCAATGCCAATG 840
QY 986 CCGTGGCTGAAAGAACGGAAGAGTTTAAGCAGAGCATTCGATTTGAGGCTTACAAAGTA 1045
Db 841 CCGTGGCTGAAAGAACGGAAGAGTTTAAGCAGAGCATTCGATTTGAGGCTTACAAAGTA 900
QY 1046 GGAACAGCACTGAGGCTCTTATGGAAGTGTGCTCCATCTGACAGAGGAATTAAT 1105
Db 901 GGAACAGCACTGAGGCTCTTATGGAAGTGTGCTCCATCTGACAGAGGAATTAAT 960
QY 1106 ACTGTGTATGAGAAATGAATACGGGTCTCATCAATCAAGTACCTGTGATGTTGTG 1165
Db 961 ACTGTGTATGAGAAATGAATACGGGTCTCATCAATCAAGTACCTGTGATGTTGTG 1020
QY 1166 GAGGATGCTCTACCGGCCATCTCTCAAGCCGGAATGCGGCAATGCTTCCACATG 1225
Db 1021 GAGGATGCTCTACCGGCCATCTCTCAAGCCGGAATGCGGCAATGCTTCCACATG 1080
QY 1226 GTGGAAGAGAGTGAAGTTGTCTGCAAGGTTTACAGTGAATGCCAGCCCACTCAG 1285
Db 1081 GTGGAAGAGAGTGAAGTTGTCTGCAAGGTTTACAGTGAATGCCAGCCCACTCAG 1140
QY 1286 TGGATCAAGCAGTGAAGAAAGACCGAGTAATACGGGCGGACGGGCTGCTCACTC 1345
Db 1141 TGGATCAAGCAGTGAAGAAAGACCGAGTAATACGGGCGGACGGGCTGCTCACTC 1200
QY 1346 AAGTTTCTCAAGCACTCGGGATTAATATGTTCCAAATGCAAGATGCTGCTGTG----- 1400
Db 1201 AAGTTTCTCAAGCAGCGCGGTGTTAAACAACGGAAGAAAGATTGAAGTTCTCATATAT 1260
QY 1401 -TCAATGTGACGAGAGCGAGTGTGGGAAATATATATGTAAGTCTCAATTAATAGG 1459
Db 1261 CGGAATGTATCTTTTGAAGAGCGTGGGAAATATATGCTGCTTGGCGGATTAATTTGG 1320
QY 1460 CAGGCCAACAGTCTGCTGCTCACTGTCTGCCAAACAGCAAGCGCTTGAAGAGAA 1519
Db 1321 ATATCTTTCACTGTGATGATGTGACAGTCTGCGC-----AGCGCTGGAAGAGAA 1371

QY	1520	AAGGAGATTACAGCTTCCCAGACTACTCTGGAGATACCAATTATCTGACATAGGGGCTTC	1579
Db	1372	AAGGAGATTACAGCTTCCCAGACTACTCTGGAGATACCAATTATCTGACATAGGGGCTTC	1431
QY	1580	TTAATCGCTGTATGTGTGTAAAGTATCTCTGTCCGAATGAAAGAACAGACCAAG	1639
Db	1432	TTAATCGCTGTATGTGTGTAAAGTATCTCTGTCCGAATGAAAGAACAGACCAAG	1491
QY	1640	CCAGACTTCAGCAGCCAGCCGGCTGTGCACAAAGTTGACCAACGATACCCCTCGCGAGA	1699
Db	1492	CCAGACTTCAGCAGCCAGCCGGCTGTGCACAAAGTTGACCAACGATACCCCTCGCGAGA	1551
QY	1700	CAGGTAAAGTTTCGGCTGAGTCCAGCTCCCTCATGAACTCCAAACCCCGCTGTGAGG	1759
Db	1552	CAGGTAAAGTTTCGGCTGAGTCCAGCTCCCTCATGAACTCCAAACCCCGCTGTGAGG	1611
QY	1760	ATTAACAACAGCCTCTCTTCAACGGCAGACACCCCATGCTGGCAGGGGCTCCGAGTAT	1819
Db	1612	ATTAACAACAGCCTCTCTTCAACGGCAGACACCCCATGCTGGCAGGGGCTCCGAGTAT	1671
QY	1820	GAACTTCCAGAGGAGCCCAAAATGGAGTTTCCAGAGATAGCTGACACTGCGCAAGCCC	1879
Db	1672	GAACTTCCAGAGGAGCCCAAAATGGAGTTTCCAGAGATAGCTGACACTGCGCAAGCCC	1731
QY	1880	CTGGAGAGAGGTTCCTTTGGGCAATGTGTCAATGGCGAAGCAGTGGAAATTGACAAAGAC	1939
Db	1732	CTGGAGAGAGGTTCCTTTGGGCAATGTGTCAATGGCGAAGCAGTGGAAATTGACAAAGAC	1791
QY	1940	AAGCCCAAGAGGCGGTCACTCGTGGCCCTTGAAAGATGTTGAAAGATGATGCCAGAGAAA	1999
Db	1792	AAGCCCAAGAGGCGGTCACTCGTGGCCCTTGAAAGATGTTGAAAGATGATGCCAGAGAAA	1851
QY	2000	GACCTTCTGATCTGTGTGACAGATGAGATGATGAAGATGATTTGGGAAACAAGAT	2059
Db	1852	GACCTTCTGATCTGTGTGACAGATGAGATGATGAAGATGATTTGGGAAACAAGAT	1911
QY	2060	ATCATTAATCTTCTTGAGACCTGCAACAAGATGGGCTCTCTATGTCTATAGTTGAATAT	2119
Db	1912	ATCATTAATCTTCTTGAGACCTGCAACAAGATGGGCTCTCTATGTCTATAGTTGAATAT	1971
QY	2120	GGCTCTAAAGGCAACCTCCGAATAACTCCGAGCCCGAGGCGCACCCGGAGTGAAGTAC	2179
Db	1972	GGCTCTAAAGGCAACCTCCGAATAACTCTCGAGCCCGAGGCGCACCCGGAGTGAAGTAC	2031
QY	2180	TCCATGACATTAAACCGTGTTCCTGAGAGACGATGACCTTCAAGACTTGTGTCTATGC	2239
Db	2032	TCCATGACATTAAACCGTGTTCCTGAGAGACGATGACCTTCAAGACTTGTGTCTATGC	2091
QY	2240	ACCTTACAGCTGGCCAGACGAGATGAGTACTTGGCTCCCAAAATGTATCATCGAGAT	2299
Db	2092	ACCTTACAGCTGGCCAGAGGCAATGAGTACTTGGCTCCCAAAATGTATCATCGAGAT	2151
QY	2300	TTAGCAGCAGAAATGTTTGGTTAACAGAAAACAATGTGATGAAATAGCAGACTTTGGA	2359
Db	2152	TTAGCAGCAGAAATGTTTGGTTAACAGAAAACAATGTGATGAAATAGCAGACTTTGGA	2211
QY	2360	CTGCGCAGAGATATCAACAATATATAGTATTAACAAAAGACCAACAAATGGCGGCTTCCA	2419
Db	2212	CTGCGCAGAGATATCAACAATATATAGTATTAACAAAAGACCAACAAATGGCGGCTTCCA	2271
QY	2420	GTCAAATGATGTGCTCAAGAGCCGTTTGTAGATGATCACTCATCAGAGTATGTC	2479
Db	2272	GTCAAATGATGTGCTCAAGAGCCGTTTGTAGATGATCACTCATCAGAGTATGTC	2331
QY	2480	TGCTCTCTCGGGGTGTAAATGTGGAGATCTTCACTTAAGGGGGCTCGCCTTACCAAGGG	2539
Db	2332	TGCTCTCTCGGGGTGTAAATGTGGAGATCTTCACTTAAGGGGGCTCGCCTTACCAAGGG	2391
QY	2540	ATTCCCGTGAAGAACTTTTAACTGTGCTGAAGAGAAAGACAGAAATGGATTAAGCAAGC	2599
Db	2392	ATTCCCGTGAAGAACTTTTAACTGTGCTGAAGAGAAAGACAGAAATGGATTAAGCAAGC	2451

OY	2600	AACCTGCACCAACCAACCTGTACATGATGTATAGAGGACCTGTGGCATGTGAGAGGCCCTCCAG	2659
Db	2452	AACCTGCACCAACCAACCTGTACATGATGTATAGAGGACCTGTGGCATGTGAGAGGCCCTCCAG	2511
OY	2660	AGACCAACGTTCCAGCAGTTGGTAGAAGACTTGGATCGAATTCTCACTCTCCACCAACAT	2719
Db	2512	AGACCAACGTTCCAGCAGTTGGTAGAAGACTTGGATCGAATTCTCACTCTCCACCAACAT	2571
OY	2720	GAGGAATACCTTGGACCTTCAGGCCACCTCTGGAACAGATTCACCTACTGTTCCCGACACA	2779
Db	2572	GAGGAATACCTTGGACCTTCAGGCCACCTCTGGAACAGATTCACCTACTGTTCCCGACACA	2631
OY	2780	AGAAGTCTTGTTCTTCAGAGAGATTCGTGTTTTCTCCAGACCCCATGCCTTACGAA	2839
Db	2632	AGAAGTCTTGTTCTTCAGAGAGATTCGTGTTTTCTCCAGACCCCATGCCTTACGAA	2691
OY	2840	CCATGCCCTTCTCAGTATCCACACATTAACGGCAGTGTATAAATAGTAATGACTGTGCT	2899
Db	2692	CCATGCCCTTCTCAGTATCCACACATTAACGGCAGTGTATAAATAGTAATGACTGTGCT	2751
OY	2900	GCTGTGCCCAACAGGACAGCAGCTGGGAACCTTAGCTACACTGACAGGGAGACCATGCC	2959
Db	2752	GCTGTGCCCAACAGGACAGCAGCTGGGAACCTTAGCTACACTGACAGGGAGACCATGCC	2811
OY	2960	TCCCAAGCTTGTGTCTCCACTTGTATATATGATCAGAGAGATTAATAATTGGAAAG	3019
Db	2812	TCCCAAGCTTGTGTCTCCACTTGTATATATGATCAGAGAGATTAATAATTGGAAAG	2871
OY	3020	TAATCAGATATGTGTAAAGATTTATACAGTTGAAAACCTTGTAATCTTCCACAGAGAG	3079
Db	2872	TAATCAGATATGTGTAAAGATTTATACAGTTGAAAACCTTGTAATCTTCCACAGAGAG	2931
OY	3080	AAGAAGTTCTCGAGCAGTGTGACTGC	3106
Db	2932	AAGAAGTTCTCGAGCAGTGTGACTGC	2958

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/ RESULT 14
/ US-10-843-641A-4626
/ Sequence 4626, Application US/10843641A
/ Publication No. US20050064454A1
/ GENERAL INFORMATION:
/ APPLICANT: Avalon Pharmaceuticals, Inc.
/ TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using
/ TITLE OF INVENTION: Signature Gene Sets
/ FILE REFERENCE: 689290-189
/ CURRENT APPLICATION NUMBER: US/10/843,641A
/ CURRENT FILING DATE: 2004-05-12
/ PRIOR APPLICATION NUMBER: US/09/873,367
/ PRIOR FILING DATE: 2001-06-05
/ PRIOR APPLICATION NUMBER: US/09/954,531
/ PRIOR FILING DATE: 2001-09-18
/ PRIOR APPLICATION NUMBER: US/09/954,536
/ PRIOR FILING DATE: 2001-09-25
/ PRIOR APPLICATION NUMBER: US/09/962,436
/ PRIOR FILING DATE: 2001-09-25
/ PRIOR APPLICATION NUMBER: US/09/962,832
/ PRIOR FILING DATE: 2001-09-25
/ PRIOR APPLICATION NUMBER: US/09/964,824
/ PRIOR FILING DATE: 2001-09-27
/ PRIOR APPLICATION NUMBER: US/09/967,768
/ PRIOR FILING DATE: 2001-09-28
/ PRIOR APPLICATION NUMBER: US/09/968,007
/ PRIOR FILING DATE: 2001-10-02
/ PRIOR APPLICATION NUMBER: US/09/969,347
/ PRIOR FILING DATE: 2001-10-02
/ PRIOR APPLICATION NUMBER: US/09/969,708
/ PRIOR FILING DATE: 2001-10-03
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 8447
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 4626
/ LENGTH: 4268
/

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TYPE: DNA
 ORGANISM: Homo sapiens
 FEATURES:
 NAME/KEY: misc. feature
 LOCATION: (1)..(4268)
 OTHER INFORMATION: n=a,l,g or c
 US-10-843-641A-4626

Query Match 89.6%; Score 2781.8; DB 10; Length 4268;
 Best Local Similarity 97.3%; Pred. No. 0;
 Matches 2887; Conservative 0; Mismatches 62; Indels 18; Gaps 5;

QY 149 CCCAAGACCACTCTGCGTTTGAAGTTCCTCCCGAACCCCGGGCTGCGCTTC 208
 DB 1 CCCAAGACCACTCTGCGTTTGAAGTTCCTCCCGAACCCCGGGCTGCGCTTC 60
 QY 209 TCCATCCGACCCACCGCGGGC-CGGGACAACAACAGTTCGCGAAGAGTTCATTC 267
 DB 61 TCCATCCGACCCACCGCGGGC-CGGGACAACAACAGTTCGCGAAGAGTTCATTC 120
 QY 268 AAGTGACTGACAGACGAC-GCAGCGCTCGGTTCTGAGCCCACTGCA-CTGAAGCA 325
 DB 121 AAGTGACTGACAGACGACGCGCGCTCGGTTCTGAGCCCACTGCAAGTGAAGCA 180
 QY 326 TTGCGGTTAGTCCATCCCTAGAGAGAGTGCAGATGGGATTACGTCCATGAGGA 385
 DB 181 TTGCGGTTAGTCCATCCCTAGAGAGAGTGCAGATGGGATTACGTCCATGAGGA 240
 QY 386 TATGAAGAGACCGGGGATTGGTACCGTACCATGTCAGTGGGGTCTTCATCTGC 445
 DB 241 TATGAAGAGACCGGGGATTGGTACCGTACCGTACCATGTCAGTGGGGTCTTCATCTGC 300
 QY 446 CTGCTGCTGTCACCATGCAACCTTGTCTGCGCGGCTCTCTTCAAGTTAGTTAG 505
 DB 301 CTGCTGCTGTCACCATGCAACCTTGTCTGCGCGGCTCTCTTCAAGTTAGTTAG 360
 QY 506 GATACCACTTAAAGCCAGAGAGCCACCAACCAATPACCAATCTCTCAACGAGAAG 565
 DB 361 GATACCACTTAAAGCCAGAGAGCCACCAACCAATPACCAATCTCTCAACGAGAAG 420
 QY 566 TACGTGGCTGCGCCAGGGAGTGCCTAGAGTGCCTGCTTGAAGAGTCCGCGT 625
 DB 421 TACGTGGCTGCGCCAGGGAGTGCCTAGAGTGCCTGCTTGAAGAGTCCGCGT 480
 QY 626 ATCAGTTGACCTAAGATGGGGTGCCTTGGGGCCCAACATAGACAAGTCTTATTTGG 685
 DB 481 ATCAGTTGACCTAAGATGGGGTGCCTTGGGGCCCAACATAGACAAGTCTTATTTGG 540
 QY 686 GAGTACTTGAAGTAAAGGGGCGCAACCTAAGACCTCCGGCTTATGCTTACTGCG 745
 DB 541 GAGTACTTGAAGTAAAGGGGCGCAACCTAAGACCTCCGGCTTATGCTTACTGCG 600
 QY 746 AATGAGCTGTAGACAGTGAACCTTGGTCTTATGAGTGAATGTCACAGATGCACTCA 805
 DB 601 AATGAGCTGTAGACAGTGAACCTTGGTCTTATGAGTGAATGTCACAGATGCACTCA 660
 QY 806 TCCGAGATGATGAGATGACACCGATGTGCGGAAGATTTGTCACTGAGAACAGTAA 865
 DB 661 TCCGAGATGATGAGATGACACCGATGTGCGGAAGATTTGTGTAGTGAACAGTAA 720
 QY 866 AACAAAGAGCACTATCTGAGACCAACAGAAAGATGGAAGAGGCTCCCATGCTG 925
 DB 721 AACAAAGAGCACTATCTGAGACCAACAGAAAGATGGAAGAGGCTCCCATGCTG 780
 QY 926 CTGCGGCAACACTGCTCAAGTTTGCCTGCGACCGGGGGAACCAATGCCAATG 985
 DB 781 CTGCGGCAACACTGCTCAAGTTTGCCTGCGACCGGGGGAACCAATGCCAATG 840
 QY 986 CCGTGGCTGAAGAAACGGGAAGAGTTTAAAGCAGAGCATGCACTTGAAGCTCAAGAT 1045
 DB 841 CCGTGGCTGAAGAAACGGGAAGAGTTTAAAGCAGAGCATGCACTTGAAGCTCAAGAT 900
 QY 1046 CGAAACAGACGAGAGCTCATTTATGGAAGAGTGTCTCCATCTGACAAAGGAATTTAT 1105

DB 901 CGAAACAGACGAGAGCTCATTTATGGAAGAGTGTCTCCATCTGACAAAGGAATTTAT 960
 QY 1106 ACCCTGTATAGTGAAGATGAATACGGGTCCATCATCAACCTACCACTGAGATGTGG 1165
 DB 961 ACCCTGTATAGTGAAGATGAATACGGGTCCATCATCAACCTACCACTGAGATGTGG 1020
 QY 1166 GAGCATGAGCTCACCGGCCCATCTCCAAAGCGGAGCTGCGGCAATGCTCCACAGT 1225
 DB 1021 GAGCATGAGCTCACCGGCCCATCTCCAAAGCGGAGCTGCGGCAATGCTCCACAGT 1080
 QY 1226 GTGAGAGAGAGTGAAGTGTGTGCAAGTTTACAGTATGCCACGCTCCATCCAG 1285
 DB 1081 GTGAGAGAGAGTGAAGTGTGTGCAAGTGTACAGTATGCCACGCTCCATCCAG 1140
 QY 1286 TGGATCAAGCAGTGAAGAAAGACGGCAGTAAATACGGGCTCGAGAGGGTGCCTACCTC 1345
 DB 1141 TGGATCAAGCAGTGAAGAAAGACGGCAGTAAATACGGGCTCGAGAGGGTGCCTACCTC 1200
 QY 1346 AAGTTCTCAAGCAGTGGGATTAATAGTTCCAAATGACAGAGTGTGCTCTGT----- 1400
 DB 1201 AAGTTCTCAAGCAGCGCGCGGTGTAAACACAGACAAAGATGAGTTCTCTATATT 1260
 QY 1401 -TCAATGTGACCGAGCGGAGTCTGGGAAATATATATATATAGTCTCCAAATTATAGG 1459
 DB 1261 CGGAATGTAACTTTGAGAGAGCTGGGAAATATAGTGTGCGGGTAAATTCTATTGGG 1320
 QY 1460 CAGGCCAACAGTGTGCTGCTCACTGTCTCTCCAAACAGCAAGCGCTTGAAGAGA 1519
 DB 1321 ATATCTTCACTGCACTGCAAGTGTGAACAGTTCTGCGC-----AGCGCTTGAAGAGA 1371
 QY 1520 AAGGAGTTAAGCTTCCCAAGACTACCTGAGATAGCACTTATGCTAGAGGGCTTC 1579
 DB 1372 AAGGAGTTAAGCTTCCCAAGACTACCTGAGATAGCACTTATGCTAGAGGGCTTC 1431
 QY 1580 TTAATGCTGTATGATGTGAACAGTCACTCTGTGCGAATGAAGAACAGCAAGAG 1639
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 DB 1492 CCAAGCTTCAAGACCGCGCTGTGCAAGCTGACCAACCTATCCCTGCGGAGA 1551
 QY 1700 CAGGTAAAGTGTGGCTGAGTCAAGCTCTCCATGAATCCCAACCGCGTGTGAG 1759
 DB 1552 CAGGTAAAGTGTGGCTGAGTCAAGCTCTCCATGAATCCCAACCGCGTGTGAG 1611
 QY 1760 ATTAACAACAGCTCTCTTCAACGCGACACCCCATGCTGCAAGGGTCTCCAGTAT 1819
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 QY 1820 GAACTTCAAGAGACCCAAATAGGAGTTTCCAAAGATAGCTGACACTGGCAAGCCC 1879
 DB 1672 GAACTTCAAGAGACCCAAATAGGAGTTTCCAAAGATAGCTGACACTGGCAAGCCC 1731
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 DB 1732 CTGGAGAAAGTGTCTTGGGGAAGTGTCAATGGGGAAGCAAGTGAATTGACAAAGAC 1791
 QY 1940 AAGCCCAAGAGAGCGGTCAACGTTGCGCTGAAGATGTTGAAGATGATCCACAGAGAA 1999
 DB 1792 AAGCCCAAGAGAGCGGTCAACGTTGCGCTGAAGATGTTGAAGATGATCCACAGAGAA 1851
 QY 2000 GACTTTCTGATCTGTCTCAAGATGAGATGATGAATGTTGGAAACAAAGAT 2059
 DB 1852 GACTTTCTGATCTGTCTCAAGATGAGATGATGAATGTTGGAAACAAAGAT 1911
 QY 2060 ATCATTAATCTCTTGAAGCTGCAACAGATGGGCTCTATATGTCAATGATGAT 2119
 DB 1912 ATCATTAATCTCTTGAAGCTGCAACAGATGGGCTCTCTATATGTCAATGATGAT 1971
 QY 2120 GCTCTAAAGCAACTCCGAGATATCTCCAGAGCCCGAGGCAACCGGAGTGAAGTAC 2179

Db 1972 GCTCTAAAGCACTCCGAGATACCTCCGAGCCCGAGGCCACCCGGAGTAGATAC 2031
Oy 2180 TCTATGACATTTAACCGTGTCTCTGAGAGAGATGATGATCTTCAAGACCTTGGTGTATGC 2239
Db 2032 TCTATGACATTTAACCGTGTCTCTGAGAGAGATGATGATCTTCAAGACCTTGGTGTATGC 2091
Oy 2240 ACTTACGACCTGGCAGACGAGTAGATCTTGGCTTCCCAAAATGATTTATCATGAGAT 2299
Db 2092 ACTTACGACCTGGCAGACGAGTAGATCTTGGCTTCCCAAAATGATTTATCATGAGAT 2151
Oy 2300 TTAGAGCCAGAAAGTTTGTGTACAGAAAACATGATGATGAATGAGACCTTGTGA 2359
Db 2152 TTAGAGCCAGAAAGTTTGTGTACAGAAAACATGATGATGAATGAGACCTTGTGA 2211
Oy 2360 CTCGCGACAGATATCAACAATATAGATTTCAAAAAGACCAACCAATGGCGCTTCCA 2419
Db 2212 CTCGCGACAGATATCAACAATATAGATTTCAAAAAGACCAACCAATGGCGCTTCCA 2271
Oy 2420 GTCAAGTGGATGGCTCCAGAAAGCCCTGTTGTATGATGATGATGATGATGATGATG 2479
Db 2272 GTCAAGTGGATGGCTCCAGAAAGCCCTGTTGTATGATGATGATGATGATGATGATG 2331
Oy 2480 TGGTCTCTGGGCTTTATATGAGAGATCTTCACTTTAGGGGGCTGGCCCTACCAAGG 2539
Db 2332 TGGTCTCTGGGCTTTATATGAGAGATCTTCACTTTAGGGGGCTGGCCCTACCAAGG 2391
Oy 2540 ATTCCCGTGGAGGACCTTTTAACTGTGCTGAGAGAGACACAGATGATGATGATGATG 2599
Db 2392 ATTCCCGTGGAGGACCTTTTAACTGTGCTGAGAGAGACACAGATGATGATGATGATG 2451
Oy 2600 AACTGCACCAACGAACTGTACATGATGATGAGGAGCTGTTGGCAGTGCCTTCCAG 2659
Db 2452 AACTGCACCAACGAACTGTACATGATGATGAGGAGCTGTTGGCAGTGCCTTCCAG 2511
Oy 2660 AGACCAAGTTCAGAGAGTGTGATGAGAGCTTGAATGCAATCTCACTCAACCAAT 2719
Db 2512 AGACCAAGTTCAGAGAGTGTGATGAGAGCTTGAATGCAATCTCACTCAACCAAT 2571
Oy 2720 GAGGATATCTGAGACTCAGCCACCTCTCGAAGCAGTATTCACCTTACCTGACACA 2779
Db 2572 GAGGATATCTGAGACTCAGCCACCTCTCGAAGCAGTATTCACCTTACCTGACACA 2631
Oy 2780 AGAAGTCTTGTCTTCAAGAGATGATCTGTTTTTCTCCAGACCCCTGCTTACGAA 2839
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Oy 2840 CCATGCTCTCTCAAGATTCACACATTAACGAGTGAATTAACATGATGATGATGATG 2899
Db 2692 CCATGCTCTCTCAAGATTCACACATTAACGAGTGAATTAACATGATGATGATGATG 2751
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Oy 3020 TATATGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3079
Db 2872 TATATGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2931
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Db 2932 AAGAAAGTTTCTGAGACAGTGAAGTGC 2958

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US-10-843-641A-6931
; Sequence 6931, Application US/10843641A
; Publication No. US20050064454A1
; GENERAL INFORMATION:
; APPLICANT: Avalon Pharmaceuticals, Inc.

;; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using
;; FILE REFERENCE: 689290-189
;; CURRENT FILING DATE: 2004-05-12
;; PRIOR APPLICATION NUMBER: US/09/873,367
;; PRIOR FILING DATE: 2001-06-05
;; PRIOR APPLICATION NUMBER: US/09/954,531
;; PRIOR FILING DATE: 2001-09-18
;; PRIOR APPLICATION NUMBER: US/09/954,456
;; PRIOR FILING DATE: 2001-09-25
;; PRIOR APPLICATION NUMBER: US/09/962,436
;; PRIOR FILING DATE: 2001-09-25
;; PRIOR APPLICATION NUMBER: US/09/962,832
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;; PRIOR APPLICATION NUMBER: US/09/964,824
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;; PRIOR APPLICATION NUMBER: US/09/967,768
;; PRIOR FILING DATE: 2001-09-28
;; PRIOR APPLICATION NUMBER: US/09/968,007
;; PRIOR FILING DATE: 2001-10-02
;; PRIOR APPLICATION NUMBER: US/09/969,347
;; PRIOR FILING DATE: 2001-10-02
;; PRIOR APPLICATION NUMBER: US/09/969,708
;; Remaining Prior Application data removed - See File Wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 8447
;; SOFTWARE: Patent version 3.0
;; SEQ ID NO 6931
;; LENGTH: 4268
;; TYPE: DNA
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: misc.feature
;; LOCATION: (1)..(4268)
;; OTHER INFORMATION: n=a,t,c,g or c
US-10-843-641A-6931

Query Match 89.6%; Score 2781.8; DB 10; Length 4268;
Best Local Similarity 97.3%; Pred. No. 0;
Matches 2887; Conservative 0; Mismatches 62; Indels 18; Gaps 5;
Oy 149 CCCAAGGACCACTCTTCCGCTTGGAGTGTCTCCCGCAACCCCGGCTGTGCTTTC 208
Db 1 CCCAAGGACCACTCTTCCGCTTGGAGTGTCTCCCGCAACCCCGGCTGTGCTTTC 60
Oy 209 TCCATCCCGACCAAGCGGAGC-CGGGACAACAAGGTGCGAGAGAGCGTTGCATTTC 267
Db 61 TCCATCCCGACCAAGCGGAGCGGGGAGCAACAGGTGCGAGAGCGTTGCATTTC 120
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Oy 326 TTGCGCGTATGTCAGTCCCGGTAGAGAGTGTGAGATGAGATTAACGTCCACATGAGA 385
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Oy 386 TATGAAAGAGACCGGGGATTGTACCGTAAACATGATGATGAGGATGATTATCTGC 445
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Oy 446 CTGCTGTGTGTCACATGCACTTGTCTGTGCGCGGCTCTCTTCAAGTTAGTTAG 505
Db 301 CTGCTGTGTGTCACATGCACTTGTCTGTGCGCGGCTCTCTTCAAGTTAGTTAG 360
Oy 506 GATACCACTTATGAGACGAGAGGACCAACCAATACCAATCTCTCAACCAAGTG 565
Db 361 GATACCACTTATGAGACGAGAGGACCAACCAATACCAATCTCTCAACCAAGTG 420
Oy 566 TACGTGTGCGCCAGGAGAGTGTGATGAGTGTGCTGTGTTGAAAGATGCGCGTG 625
Db 421 TACGTGTGCGCCAGGAGAGTGTGATGAGTGTGCTGTGTTGAAAGATGCGCGTG 480

QY 626 ATCACTTGAAGCTAAGATGGGGTGCATTTGGGGCCCAACATAGACAGTGTCTTAATTGGG 685
DB 481 ATCACTTGAAGCTAAGATGGGGTGCATTTGGGGCCCAACATAGACAGTGTCTTAATTGGG 540
QY 686 GAGTCTTGACATTAAGGGGCGCAACCTAGAGACTCCGGCTCTATGCTGTGACTGGC 745
DB 541 GAGTCTTGACATTAAGGGGCGCAACCTAGAGACTCCGGCTCTATGCTGTGACTGGC 600
QY 746 ACTAGGACTGTAGACAGTGAACCTTGCTTCACTGTGATGATGTCACAGATGCCATCTCA 805
DB 601 ACTAGGACTGTAGACAGTGAACCTTGCTTCACTGTGATGATGTCACAGATGCCATCTCA 660
QY 806 TCCGAGATGATGAGATGACACCCGATGTGCGGAAGATTTTGTCACTGTGAAGCACTAAC 865
DB 661 TCCGAGATGATGAGATGACACCCGATGTGCGGAAGATTTTGTCACTGTGAAGCACTAAC 720
QY 866 AACAGAGAGCAACATCTGAGCAACAGAGAAAGATGAAAGCGGCTCCATGCTGTG 925
DB 721 AACAGAGAGCAACATCTGAGCAACAGAGAAAGATGAAAGCGGCTCCATGCTGTG 780
QY 926 CCTGCGGCCAACACTGTCAAGTTTCGCTGCCAGCCGGGGGAAACCAATGCGAACATG 985
DB 781 CCTGCGGCCAACACTGTCAAGTTTCGCTGCCAGCCGGGGGAAACCAATGCGAACATG 840
QY 986 CCGTGTCTGAAGAAACCGGAAAGATTTAAGCAGAGACATCGCATTTGAGAGCTTCAAGATA 1045
DB 841 CCGTGTCTGAAGAAACCGGAAAGATTTAAGCAGAGACATCGCATTTGAGAGCTTCAAGATA 900
QY 1046 CGAAGACAGACATGAGCCTCATTTAAGAAAGTGTGCTCCATCTGACAAAGGAAATTAAT 1105
DB 901 CGAAGACAGACATGAGCCTCATTTAAGAAAGTGTGCTCCATCTGACAAAGGAAATTAAT 960
QY 1106 ACTGTGTAGTGAAGATGAATACGGGTCATCATCAACAGTCCACCTGAGTGTGTG 1165
DB 961 ACTGTGTAGTGAAGATGAATACGGGTCATCATCAACAGTCCACCTGAGTGTGTG 1020
QY 1166 GAGCGATCGCTTCAACGGCCCATCTTCAAGCCGAGCTGCGCAAAATGCTTCAACAGT 1225
DB 1021 GAGCGATCGCTTCAACGGCCCATCTTCAAGCCGAGCTGCGCAAAATGCTTCAACAGT 1080
QY 1226 GTCCGAGGAGAGTGAAGTTTGTCTGCAAGTTTACAGTATGCCAGGCCCAACATCCAG 1285
DB 1081 GTCCGAGGAGAGTGAAGTTTGTCTGCAAGTTTACAGTATGCCAGGCCCAACATCCAG 1140
QY 1286 TGGATCAAGCAGTGTGAAGAAAGACGAGTAAATACGGGCCGAGCTGCTTCACTTC 1345
DB 1141 TGGATCAAGCAGTGTGAAGAAAGACGAGTAAATACGGGCCGAGCTGCTTCACTTC 1200
QY 1346 AAGTTTCTCAAGCATCGGGGATTAATGTTCCATATGCAAGAGTGTGCTGTG----- 1400
DB 1201 AAGTTTCTCAAGCCCGCGGTGTTAACACCAGGACAAAGATGAGGTTCTCTAATAT 1260
QY 1401 -TCAATGTAACGAGGCGAGATGCTGGGGAATATATATGTAAGTCTCCAAATATATAGGG 1459
DB 1261 CGGAATGTACTTTAAGACGCTGGGGAATATACGTGTGCGGGTATTTCTATTGGG 1320
QY 1460 CAGGCAACAGTGTGCTGCTGCTCACTGTCTGCAAAACAGCAAGCGGCTGTGAGAGAA 1519
DB 1321 AATATCTTTCACTGTGATGTTGACAGTCTTGC-----AAGGCTGTGAGAGAA 1371
QY 1520 AAGAGATTAACAGCTTCCCAAGACTACCTGTGAGATGCGCATTTACTGTGATAGGGGTCTTC 1579
DB 1372 AAGAGATTAACAGCTTCCCAAGACTACCTGTGAGATGCGCATTTACTGTGATAGGGGTCTTC 1431
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Search completed: October 2, 2006, 18:59:47
Job time : 3260 secs

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 2, 2006, 17:59:37 ; Search time 1091 Seconds
(without alignments)
5253.440 Million cell updates/sec

Title: US-10-701-263-1

Perfect score: 3106

Sequence: 1 cccgcgagcaaatgttggtg.....ttctcgagcagtgactgc 3106

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 2370645 seqs, 922650133 residues

Total number of hits satisfying chosen parameters: 4741290

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications NA New.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3025.4	97.4	4612	6	US-10-669-920-566 Sequence 566, App
2	3025.4	97.4	5003	6	US-10-669-920-572 Sequence 572, App
3	2967.4	95.5	4485	6	US-10-669-920-614 Sequence 614, App
4	2890.2	93.1	4609	6	US-10-669-920-576 Sequence 576, App
5	2890.2	93.1	5000	6	US-10-669-920-564 Sequence 564, App
6	2882.2	92.8	4990	6	US-10-669-920-634 Sequence 634, App
7	2867.8	92.3	4607	6	US-10-669-920-608 Sequence 608, App
8	2867.8	92.3	4498	6	US-10-669-920-590 Sequence 590, App
9	2824.2	90.9	4472	6	US-10-669-920-590 Sequence 590, App
10	2780.2	89.5	5080	6	US-10-669-920-598 Sequence 598, App
11	2765.8	89.0	4697	6	US-10-669-920-600 Sequence 600, App
12	2765.8	89.0	5088	6	US-10-669-920-582 Sequence 582, App
13	2641.4	85.0	3241	6	US-10-669-920-602 Sequence 602, App
14	2641.4	85.0	3632	6	US-10-669-920-626 Sequence 626, App
15	2506.2	80.7	3238	6	US-10-669-920-570 Sequence 570, App
16	2506.2	80.7	3639	6	US-10-669-920-620 Sequence 620, App
17	2506	80.7	3216	8	US-11-266-748A-30641 Sequence 30641, A
18	2425	78.1	4218	6	US-10-669-920-588 Sequence 588, App
19	2417	77.8	4208	6	US-10-669-920-606 Sequence 606, App
20	2347.8	75.6	4342	6	US-10-669-920-610 Sequence 610, App
21	2347.8	75.6	4733	6	US-10-669-920-604 Sequence 604, App
22	2327.4	74.9	4257	6	US-10-669-920-616 Sequence 616, App
23	2327.4	74.9	4646	6	US-10-669-920-594 Sequence 594, App

24	2327	74.9	4267	6	US-10-669-920-612 Sequence 612, App
25	2327	74.9	4658	6	US-10-669-920-624 Sequence 624, App
26	2319	74.7	4257	6	US-10-669-920-578 Sequence 578, App
27	2319	74.7	4648	6	US-10-669-920-586 Sequence 586, App
28	2269.4	73.1	4130	6	US-10-669-920-630 Sequence 630, App
29	2269	73.1	4140	6	US-10-669-920-622 Sequence 622, App
30	2261	72.8	4130	6	US-10-669-920-568 Sequence 568, App
31	2092.4	67.4	2657	3	US-10-669-920-592 Sequence 592, App
32	2092.4	67.4	3048	6	US-10-669-920-584 Sequence 584, App
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34	1898.2	61.1	3104	6	US-10-669-920-581 Sequence 581, App
35	1441.6	46.4	1828	6	US-10-669-920-574 Sequence 574, App
36	1441.6	46.4	2219	6	US-10-669-920-596 Sequence 596, App
37	1110.8	35.8	3809	8	US-11-266-748A-354004 Sequence 354004, A
38	1110.8	35.8	3809	8	US-11-266-748A-384732 Sequence 384732, A
39	1110.8	35.8	3809	8	US-11-266-748A-437383 Sequence 437383, A
40	1102.6	35.5	2011	6	US-10-669-920-580 Sequence 580, App
41	1102.6	35.5	2402	6	US-10-669-920-632 Sequence 632, App
42	1078.2	34.7	1882	8	US-11-266-748A-185251 Sequence 185251, A
43	1068	34.4	3722	6	US-10-669-920-432 Sequence 432, App
44	1054.4	33.9	3573	6	US-10-669-920-423 Sequence 423, App
45	1045.8	33.7	3203	6	US-10-669-920-425 Sequence 425, App

ALIGNMENTS

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RESULT 1
US-10-669-920-566
; Sequence 566, Application US/10669920
; Publication No. US20060194265A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
; APPLICANT: Malandro, Marc S.
; TITLE OF INVENTION: NOVEL THERAPEUTIC TARGETS IN CANCER
; FILE REFERENCE: 20366-066001
; CURRENT APPLICATION NUMBER: US/10/669,920
; CURRENT FILING DATE: 2003-09-23
; PRIOR APPLICATION NUMBER: US 10/004,113
; PRIOR FILING DATE: 2001-10-23
; PRIOR APPLICATION NUMBER: US 10/052,482
; PRIOR FILING DATE: 2001-11-08
; PRIOR APPLICATION NUMBER: US 09/997,722
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: US 10/034,650
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: US 10/085,117
; PRIOR FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: US 10/087,192
; PRIOR FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 10/322,281
; PRIOR FILING DATE: 2002-12-17
; PRIOR APPLICATION NUMBER: US 10/322,696
; PRIOR FILING DATE: 2002-12-17
; NUMBER OF SEQ ID NOS: 1441
; SOFTWARE: FastSeq for Windows Version 4.0
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; LENGTH: 4612
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-669-920-566

Query Match      97.4%; Score 3025.4; DB 6; Length 4612;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 3100; Conservative 0; Mismatches 6; Indels 11; Gaps 6;

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Qy	2750	GAAACGATATCACTAGATTACCTGTACACAGAGTTCTTGTCTTCAGAGATGATTTCT	2800
Db	2947	GAAACGATATCACTAGATTACCTGTACACAGAGTTCTTGTCTTCAGAGATGATTTCT	3000
Qy	2810	GTTTTTTTCTCCAGAACCCCATGGCTTACGAACCATGCTTCCATGATTCACACATTAAC	2866
Db	3007	GTTTTTTTCTCCAGAACCCCATGGCTTACGAACCATGCTTCCATGATTCACACATTAAC	3066
Qy	2870	GGCAGTGTAAAAACATGATGACTGTGTGCTGCTGCCCAACACAGACAGCATGGGAA	2922
Db	3067	GGCAGTGTAAAAACATGATGACTGTGTGCTGCTGCCCAACACAGACAGCATGGGAA	3122
Qy	2930	CTTACTCACTGACAGGAGGAGACCAATGCTCCAGAGCTTGTGTCTCACTGTATAT	2988
Db	3127	CTTACTCACTGACAGGAGGAGACCAATGCTCCAGAGCTTGTGTGTCTCACTGTATAT	3188
Qy	2990	ATGATCAAGAGAGTAAATATTTGAAAAATGATACGCTATGTGTAAAGATTTATACAG	3044
Db	3187	ATGATCAAGAGAGTAAATATTTGAAAAATGATACGCTATGTGTAAAGATTTATACAG	3244
Qy	3050	TTGAAAACCTGTAACTCTCCCAAGAGGAGAAAGGTTCTGGAGCAGTGCCTG	3106
Db	3247	TTGAAAACCTGTAACTCTCTCCCAAGAGGAGAAAGGTTCTGGAGCAGTGCCTG	3303
RESULT 2			
US-10-669-920-572			
/ Sequence 572, Application US/10669920			
/ Publication No. US20060194265A1			
/ GENERAL INFORMATION:			
/ APPLICANT: Moritz, David W.			
/ APPLICANT: Malandro, Marc S.			
/ TITLE OF INVENTION: NOVEL THERAPEUTIC TARGETS IN CANCER			
/ FILE REFERENCE: 20366-066001			
/ CURRENT APPLICATION NUMBER: US/10/669,920			
/ CURRENT FILING DATE: 2003-09-23			
/ PRIOR APPLICATION NUMBER: US 10/004,113			
/ PRIOR FILING DATE: 2001-10-23			
/ PRIOR APPLICATION NUMBER: US 10/052,482			
/ PRIOR FILING DATE: 2001-11-08			
/ PRIOR APPLICATION NUMBER: US 09/997,722			
/ PRIOR FILING DATE: 2001-11-30			

	Query Match	97.4%	Score 3025.4	DB 6	Length 5003	
	Best Local Similarity	99.5%	Pred. No. 0			
	Matches 3100	Conservative	0	Mismatches	6	Indels 11; Gaps 6;
QY	1	CCCCGAGCAAAAGTTTGATGAGGACAAG-C-CAAGCTGAAGTCTTTCTTCTCTGTTCC	59			
DB	578	CTCCGAGCAAAAGTTTGATGAGGACAAGCAAGCTGAAGTCTTTCTTCTCTGTTCC	637			
QY	60	CCAAATCCGAGGAGCAGCCCGGGGCTGATG--GCGCTCTCCGAGGCTGGGGTACGC	116			
DB	638	CCAAATCCGAGGAGCAGCCCGGGGCTGATG--GCGCTCTCCGAGGCTGGGGTACGC	697			
QY	117	GTGAAGCCCGGGAAGGCTTGGGCGCGGAGAGACCAGAGACCACTCTTCTGCTTGGAG	176			
DB	698	GTGAAGCCCGGGAAGGCTTGGGCGCGGAGAGACCAGAGACCACTCTTCTGCTTGGAG	757			
QY	177	TTGCTCCCGGCAACCCCGGAGCTCGTCGCTTTCTTCATCCCGACCAGCGGGAGC-CGGAG	235			
DB	758	TTGCTCCCGGCAACCCCGGAGCTCGTCGCTTTCTTCATCCCGACCAGCGGGAGC-CGGAG	817			
QY	236	ACAACACAGGTGCGGAGAGAGCGTTGCCATTCAAGTATCTGCAGACAGACG-CGAGCGCC	294			
DB	818	ACAACACAGGTGCGGAGAGAGCGTTGCCATTCAAGTATCTGCAGACAGACGCGAGCGGCC	877			
QY	295	TTCGGTTTCTGAGCCCAACCGCA-GCTGAAGGCAATTGGCGGATGATGCCCGGTAGAGAA	353			
DB	878	TTCGGTTTCTGAGCCCAACCGCAAGCTGAAGGATGGCGGTATGATCAAGCCCGTAGAGAA	937			
QY	354	GTGAGCAGATGGATTTAAGTCACAATGAGATATGGAAGAGACCGGGAGTTGTATCG	413			
DB	938	GTGAGCAGATGGATTTAAGTCACAATGAGATATGGAAGAGACCGGGAGTTGTATCG	997			
QY	414	TAAACATGTCAGCTGGGGGTGTTTCATCTGCTGTCGTGTCATCCATGCGCAACTTGT	473			
DB	998	TAAACATGTCAGCTGGGGGTGTTTCATCTGCTGTCGTGTCATCCATGCGCAACTTGT	1057			
QY	474	CCCTGGCCCGGCTCTCTTCAAGTTAGTTAGATATCAACATTTAGAGCGAAGAGCCAC	533			
DB	1058	CCCTGGCCCGGCTCTCTTCAAGTTAGTTAGATATCAACATTTAGAGCGAAGAGCCAC	1117			
QY	534	CAACCAAAATACCAATCTCTCAACACAGAGTATGTCGTCGCCCAAGGAGTGCCTAG	593			
DB	1118	CAACCAAAATACCAATCTCTCAACACAGAGTATGTCGTCGCCCAAGGAGTGCCTAG	1177			
QY	594	AGGTGCGGTGCTTGTGAAGATGCGCGCTGATCAAGTTGAGCTAAGGATGGGTGACT	653			
DB	1178	AGGTGCGGTGCTTGTGAAGATGCGCGCTGATCAAGTTGAGCTAAGGATGGGTGACT	1237			
QY	654	TGGGCGCCCAAAATAGACAGTGTATATTTGGGAGATCTTGCAATTAAGGCGCCACAC	713			
DB	1238	TGGGCGCCCAAAATAGACAGTGTATATTTGGGAGATCTTGCAATTAAGGCGCCACAC	1297			
QY	714	CTAGAGACTCGGCGCTCTATGCTTGTACTGCAATAGGACTGTATGACAGTGAACCTTGGT	773			
DB	1298	CTAGAGACTCGGCGCTCTATGCTTGTACTGCAATAGGACTGTATGACAGTGAACCTTGGT	1357			

OY 774 ACTTCATGTGAATGTCAAGATGTCATCTCATCCGAGATGATGAGGATGACACCGATG 833
DB 1358 ACTTCATGTGAATGTCAAGATGTCATCTCATCCGAGATGATGAGGATGACACCGATG 1417
OY 834 GTGCGGAAGATTTGTCTGATGAGAACAGTAAACAAAGAGACCAATCTGAGACCAAC 893
DB 1418 GTGCGGAAGATTTGTCTGATGAGAACAGTAAACAAAGAGACCAATCTGAGACCAAC 1477
OY 894 CAGAAAAGATGGAAGAGGAGCTCACTGCTGCTGAGCCGAGCAACCTGCAAGTTGCT 953
DB 1478 CAGAAAAGATGGAAGAGGAGCTCACTGCTGCTGAGCCGAGCAACCTGCAAGTTGCT 1537
OY 954 GCCCAGCCGAGGAGGAGCCCAATGCCCAACCATGCGGTGCTGAAAACCGGAAAGATT 1013
DB 1538 GCCCAGCCGAGGAGGAGCCCAATGCCCAACCATGCGGTGCTGAAAACCGGAAAGATT 1597
OY 1014 AGCAGAGCATGCGATTTGAGAGCTACAGAGTACGAACCAAGCATGAGCTCATTTATG 1073
DB 1598 AGCAGAGCATGCGATTTGAGAGCTACAGAGTACGAACCAAGCATGAGCTCATTTATG 1657
OY 1074 AAAGTGTGTCCCATCTGACAAAGGGAATTAACCTGTGTGTGAGCGATCGCTCAAC 1133
DB 1658 AAAGTGTGTCCCATCTGACAAAGGGAATTAACCTGTGTGTGAGCGATCGCTCAAC 1717
OY 1134 CCATCAATCACACGTACCACTGATGTGTGTGAGCGATCGCTCAACCGCCCATCTCC 1193
DB 1718 CCATCAATCACACGTACCACTGATGTGTGTGAGCGATCGCTCAACCGCCCATCTCC 1777
OY 1194 AAAGCGGAGCTGCGGCAAAATGCTTCACAGTGTGTGAGAGAGAGTAAAGTTGTCTCA 1253
DB 1778 AAAGCGGAGCTGCGGCAAAATGCTTCACAGTGTGTGAGAGAGAGTAAAGTTGTCTCA 1837
OY 1254 AGGTTTACAGTATGCCAGGCCCAATCACTGATGTGTGAGAGAGAGTAAAGTTGTCTCA 1313
DB 1838 AGGTTTACAGTATGCCAGGCCCAATCACTGATGTGTGAGAGAGAGTAAAGTTGTCTCA 1897
OY 1314 GTAAATACGAGGAGCGGAGCTGCTCACTCAAGGTTCTCAAGCATGCGGGAATTA 1373
DB 1898 GTAAATACGAGGAGCGGAGCTGCTCACTCAAGGTTCTCAAGCATGCGGGAATTA 1957
OY 1374 GTTCCATGACAGATGCTGCTGCTGTTCAATGTGACCGAGGCGGATGCTGGGGAATTA 1433
DB 1958 GTTCCATGACAGATGCTGCTGCTGTTCAATGTGACCGAGGCGGATGCTGGGGAATTA 2017
OY 1434 TATGTAAAGTCTCAATTTATATAGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1493
DB 2018 TATGTAAAGTCTCAATTTATATAGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2077
OY 1494 CAAAACAGCAGAGCGCTGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1553
DB 2078 CAAAACAGCAGAGCGCTGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2137
OY 1554 TAGCCATTTACTGATAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1613
DB 2138 TAGCCATTTACTGATAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2197
OY 1614 GCGGATGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1673
DB 2198 GCGGATGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2257
OY 1674 TGACCAAAAGTATCCCTGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1729
DB 2258 TGACCAAAAGTATCCCTGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2317
OY 1730 TCCATGAACTCCAAACCCCGCTGTGTGAGGATTAACAACGCTCTCTTCAACGAGAGC 1789
DB 2318 TCCATGAACTCCAAACCCCGCTGTGTGAGGATTAACAACGCTCTCTTCAACGAGAGC 2377
OY 1790 ACCCCATGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1849
DB 2378 ACCCCATGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2437

OY 1850 CCAAGATTAAGCTGACATGCGGCAAGCCCTGAGGAGAAAGTTGCTTTGGCAAGTGTG 1909
DB 2438 CCAAGATTAAGCTGACATGCGGCAAGCCCTGAGGAGAAAGTTGCTTTGGCAAGTGTG 2497
OY 1910 ATGGCGGAACAGTGGAGATTGACAAAGACAAAGGAGGAGGAGGAGGAGGAGGAGGAG 1969
DB 2498 ATGGCGGAACAGTGGAGATTGACAAAGACAAAGGAGGAGGAGGAGGAGGAGGAGGAG 2557
OY 1970 AAGATTTGAAGATGATGACCAAGAGAAAGACCTTTCTGATCTGTGTGTGAGATGAG 2029
DB 2558 AAGATTTGAAGATGATGACCAAGAGAAAGACCTTTCTGATCTGTGTGTGAGATGAG 2617
OY 2030 ATGATGAAGATGATGAGGAGAAACAAAGATATCAATAATCTTTGAGAGCTGACACAG 2089
DB 2618 ATGATGAAGATGATGAGGAGAAACAAAGATATCAATAATCTTTGAGAGCTGACACAG 2677
OY 2090 GATGGGCTCTCTATGTCAATGATGATGATGATGATGATGATGATGATGATGATGATG 2149
DB 2678 GATGGGCTCTCTATGTCAATGATGATGATGATGATGATGATGATGATGATGATGATG 2737
OY 2150 CAGAGCCGAGAGGAGCCCGGAGATGAGTACTCTATGACATTAACGCTGTCTGAGAGAG 2209
DB 2738 CAGAGCCGAGAGGAGCCCGGAGATGAGTACTCTATGACATTAACGCTGTCTGAGAGAG 2797
OY 2210 CAGATGACCTTCAAGGACTTGTGTGATGACCTTACCAAGCTGAGCAGAGGAGTGAATG 2269
DB 2798 CAGATGACCTTCAAGGACTTGTGTGATGACCTTACCAAGCTGAGCAGAGGAGTGAATG 2857
OY 2270 TTGGCTTCCCAAAATGATTTATCATGAGATTTAGACAGCAAAATGTTTGTGTAACAGAA 2339
DB 2858 TTGGCTTCCCAAAATGATTTATCATGAGATTTAGACAGCAAAATGTTTGTGTAACAGAA 2917
OY 2330 AACATGTGATGAATAATGACAGCTTTGAGCTGCGCAGAGATATCAACATATGACTAT 2389
DB 2918 AACATGTGATGAATAATGACAGCTTTGAGCTGCGCAGAGATATCAACATATGACTAT 2977
OY 2390 TACAAAAGACCAACCAATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2449
DB 2978 TACAAAAGACCAACCAATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3037
OY 2450 GATAGATATACACTCATCAAGTATGATGATGATGATGATGATGATGATGATGATGATG 2509
DB 3038 GATAGATATACACTCATCAAGTATGATGATGATGATGATGATGATGATGATGATGATG 3097
OY 2510 TTCACTTAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2569
DB 3098 TTCACTTAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3157
OY 2570 AAGGAAGGACAGAGATGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2629
DB 3158 AAGGAAGGACAGAGATGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3217
OY 2630 AAGGAGCTGTGAGTATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2689
DB 3218 AAGGAGCTGTGAGTATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3277
OY 2690 TTGATGCAATTTCTCATCTCTCAACCAATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2749
DB 3278 TTGATGCAATTTCTCATCTCTCAACCAATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3337
OY 2750 GAAAGATTTTCAACCTAGTAACTCTGAGCAAGAGGAGGAGGAGGAGGAGGAGGAGGAG 2809
DB 3338 GAAAGATTTTCAACCTAGTAACTCTGAGCAAGAGGAGGAGGAGGAGGAGGAGGAGGAG 3397
OY 2810 GTTTTCTTCCAGAGCCCATGCTTACCAAGCAATGCTTCTCAATATCAACATAAAC 2869
DB 3398 GTTTTCTTCCAGAGCCCATGCTTACCAAGCAATGCTTCTCAATATCAACATAAAC 3457
OY 2870 GGCAGTGTAAACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2929
DB 3458 GGCAGTGTAAACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3517
OY 2930 CCTACTACACTGAGCAAGGAGACCATGCTTCCAGAGCTGTGTCTTCACTTATATAT 2989

Db 3518 CCTACTACTGAGGAGGAGACATGCTCCGAGCTTTCTTCCACTTTGTAAT 3577
 Qy 2990 ATGATCAGAGAGTAATATATATGAAAAAGTAATCAGATATGTGTAAGATTATACG 3049
 Db 3578 ATGATCAGAGAGTAATATATATGAAAAAGTAATCAGATATGTGTAAGATTATACG 3637
 Qy 3050 TTGAAACTTGTATCTTCCCGAGAGAAAGAGTTTCTGAGCAGTGAATGCG 3106
 Db 3638 TTGAAACTTGTATCTTCCCGAGAGAAAGAGTTTCTGAGCAGTGAATGCG 3694

RESULT 3

US-10-669-920-614
 ; Sequence 614, Application US/10669920
 ; Publication No. US20060194265A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Morita, David W.
 ; APPLICANT: Malandro, Marc S.
 ; TITLE OF INVENTION: NOVEL THERAPEUTIC TARGETS IN CANCER
 ; FILE REFERENCE: 20366-066001
 ; CURRENT APPLICATION NUMBER: US/10/669,920
 ; PRIOR FILING DATE: 2003-09-23
 ; PRIOR APPLICATION NUMBER: US 10/004,113
 ; PRIOR FILING DATE: 2001-10-23
 ; PRIOR APPLICATION NUMBER: US 10/052,482
 ; PRIOR FILING DATE: 2001-11-08
 ; PRIOR APPLICATION NUMBER: US 09/997,722
 ; PRIOR FILING DATE: 2001-11-30
 ; PRIOR APPLICATION NUMBER: US 10/034,650
 ; PRIOR FILING DATE: 2001-12-20
 ; PRIOR APPLICATION NUMBER: US 10/085,117
 ; PRIOR FILING DATE: 2002-02-27
 ; PRIOR APPLICATION NUMBER: US 10/087,192
 ; PRIOR FILING DATE: 2002-03-01
 ; PRIOR APPLICATION NUMBER: US 10/322,281
 ; PRIOR FILING DATE: 2002-12-17
 ; PRIOR APPLICATION NUMBER: US 10/322,696
 ; PRIOR FILING DATE: 2002-12-17
 ; NUMBER OF SEQ ID NOS: 1441
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 614
 ; LENGTH: 4485
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-10-669-920-614

Query Match 95.5%; Score 2967.4; DB 6; Length 4485;
 Best Local Similarity 99.4%; Pired. No. 0;
 Matches 3042; Conservative 0; Mismatches 6; Indels 11; Gaps 6;
 Qy 1 CCGGAGAGAAAGTTGTGTGAGGCAAG-CAAGCTGAGTCTTCTCTCTCGTTCC 59
 Db 578 CTGCGAGCAAGTTGTGTGAGGCAACGCAAGCTGAGTCTTCTCTCTCGTTCC 637
 Qy 60 CCAAAATCGAGGCGAGCCGCGGCGGTCAATG--GCGTCTCTCGGAGGCTGGGTAACG 116
 Db 638 CCAAAATCGAGGCGAGCCGCGGCGGTCAATG--GCGTCTCTCGGAGGCTGGGTAACG 697
 Qy 117 GTGAAACCCCGGAGGCTTGGCGCGGCGAAGACCAAGACCACTCTGCGTTGAG 176
 Db 698 GTGAAACCCCGGAGGCTTGGCGCGGCGAAGACCAAGACCACTCTGCGTTGAG 757
 Qy 177 TTGCTCCCGCAACCCCGGCGTGTGCTTCTCAATCCGACCAAGCGGAGGCG-CGGAG 235
 Db 758 TTGCTCCCGCAACCCCGGCGTGTGCTTCTCAATCCGACCAAGCGGAGGCGGAGG 817
 Qy 236 ACAACAAGGTGCGGAGAGGCTTGCATTGAAGTGTGAGAGAGC-AGAGGCGC 294
 Db 818 ACAACAAGGTGCGGAGAGGCTTGCATTGAAGTGTGAGAGAGCAGCGGCGC 877
 Qy 295 TCGGTTCTGAGGCGCAACCGCA-GCTGAAGGCAATTGGCGTGAAGCAATGCCGTAAGAGAA 353

Db 878 TCGGTTCTGAGGCGCAACCGGAGGCTGAAGGCAATGCGGTAGTCATCCCGTAAAGAA 937
 Qy 354 GTGCGCAATGGAATTAAGTCCATAGAGATATGAAAGAGACCGGGAGTTGGTACCG 413
 Db 938 GTGCGCAATGGAATTAAGTCCATAGAGATATGAAAGAGACCGGGAGTTGGTACCG 997
 Qy 414 TAAACATGATGAGCTGGGGTGGTTTCAATCTGCTGTGTGTGTCACATGCGAATCTGT 473
 Db 998 TAAACATGATGAGCTGGGGTGGTTTCAATCTGCTGTGTGTGTCACATGCGAATCTGT 1057
 Qy 474 CCTGGCCCGGCGCTCTTCAAGTTAGTTGAGAGATCAACATTAGAGCCAAAGGCCAC 533
 Db 1058 CCTGGCCCGGCGCTCTTCAAGTTAGTTGAGAGATCAACATTAGAGCCAAAGGCCAC 1117
 Qy 534 CAACCAATTAACCAATCTCTCAACCAAGAGTATAGTGGCTGCGCAGGGAGTGCTAG 593
 Db 1118 CAACCAATTAACCAATCTCTCAACCAAGAGTATAGTGGCTGCGCAGGGAGTGCTAG 1177
 Qy 594 AGTGCCTGCTGTTGAAAGATGCGCGCGGATCAATGGAATGAGATGAGGCTGACT 653
 Db 1178 AGTGCCTGCTGTTGAAAGATGCGCGCGGATCAATGGAATGAGATGAGGCTGACT 1237
 Qy 654 TGGGCGCCCAATATGAGCAGTGTATTGAGGAGTACTTGCAATTAAGGCGCCACAC 713
 Db 1238 TGGGCGCCCAATATGAGCAGTGTATTGAGGAGTACTTGCAATTAAGGCGCCACAC 1297
 Qy 714 CTAGAGACTCGGCGCTTATGTTGTATCTGCGAGTATGAGTGTAGACATGTAACCTGGT 773
 Db 1238 CTAGAGACTCGGCGCTTATGTTGTATCTGCGAGTATGAGTGTAGACATGTAACCTGGT 1357
 Qy 774 ACTCATGATGATATGTCACAGATGCAATCTCATCCGAGATGATGAGTATGACACGATG 833
 Db 1358 ACTCATGATGATATGTCACAGATGCAATCTCATCCGAGATGATGAGTATGACACGATG 1417
 Qy 834 GTGCGAAGATTTTGTCAATGAGAAAGTATCAACAAGAGACCAATATCTGAGCCACA 893
 Db 1418 GTGCGAAGATTTTGTCAATGAGAAAGTATCAACAAGAGACCAATATCTGAGCCACA 1477
 Qy 894 CAGAAAGATGAAAGGCGCTTCATGCTGTGCTCGCGGCAACATGTCAGATTTGGCT 953
 Db 1478 CAGAAAGATGAAAGGCGCTTCATGCTGTGCTCGCGGCAACATGTCAGATTTGGCT 1537
 Qy 954 GCCGAGCGGGGGGAAACCAATGCCAATCCATGCGGTGCTGAAAAACGGAGAGGTTTA 1013
 Db 1538 GCCGAGCGGGGGGAAACCAATGCCAATCCATGCGGTGCTGAAAAACGGAGAGGTTTA 1597
 Qy 1014 AGCAGAGCATGCAATGAGGCTCAAGATACGAAACCAAGCATGAGACCTCATATTAG 1073
 Db 1598 AGCAGAGCATGCAATGAGGCTCAAGATACGAAACCAAGCATGAGACCTCATATTAG 1657
 Qy 1074 AAAGTGTGCTCCATCTGCAAGAGGAAATTAATCTGTGTATGAGAAATGAATCGGGT 1133
 Db 1658 AAAGTGTGCTCCATCTGCAAGAGGAAATTAATCTGTGTATGAGAAATGAATCGGGT 1717
 Qy 1134 CCATCAATCAAGATACCACTGATGTTGTGAGAGCATGCGCTCAACCGGCCCATCTCC 1193
 Db 1718 CCATCAATCAAGATACCACTGATGTTGTGAGAGCATGCGCTCAACCGGCCCATCTCC 1777
 Qy 1194 AAGCGGAGCTGCGGCAATATGCTTCCACAGTGTGTGAGAGAGACGTAAGTTTCTGCA 1253
 Db 1778 AAGCGGAGCTGCGGCAATATGCTTCCACAGTGTGTGAGAGAGACGTAAGTTTCTGCA 1837
 Qy 1254 AGTTTATCAGTATGCTCCAGCCCAATCCATGATGATCAAGACGAGGAAAGAACGGCA 1313
 Db 1838 AGTTTATCAGTATGCTCCAGCCCAATCCATGATGATCAAGACGAGGAAAGAACGGCA 1897
 Qy 1314 GTAATATAGGAGCGGAGGCTGCTCACTCAAGTTTCTCAAGCACTCGGGATTAATA 1373
 Db 1898 GTAATATAGGAGCGGAGGCTGCTCACTCAAGTTTCTCAAGCACTCGGGATTAATA 1957
 Qy 1374 GTTCCAAATCAGAAAGTGTGCTGTGTAATGTGACGAGGCGGATGCTGGAGAAATATA 1433
 Db 1958 GTTCCAAATCAGAAAGTGTGCTGTGTAATGTGACGAGGCGGATGCTGGAGAAATATA 2017

1434 TATGTAAAGTCTCCAAATTATATAGGGCAGGCCCAACCAAGTCTGCTGCTCACTGTCTGC 1493
1434 TATGTAAAGTCTCCAAATTATATAGGGCAGGCCCAACCAAGTCTGCTGCTCACTGTCTGC 1493
2018 TATGTAAAGTCTCCAAATTATATAGGGCAGGCCCAACCAAGTCTGCTGCTCACTGTCTGC 2077
1494 CAAAACAGCAGCGCTTGGAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 1553
2078 CAAAACAGCAGCGCTTGGAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 2137
1554 TAGCCATTACTGATAGAGGGCTCTTAAATGCGCTGATGAGTGAACAGTCAATCTCTGT 1613
2138 TAGCCATTACTGATAGAGGGCTCTTAAATGCGCTGATGAGTGAACAGTCAATCTCTGT 2197
1614 GCCGATGAAGAAACGACCAAGAAACCAAGACTTCAAGCCAGCCGCTGTGCAAGC 1673
2198 GCCGATGAAGAAACGACCAAGAAACCAAGACTTCAAGCCAGCCGCTGTGCAAGC 2257
1674 TGACCAAACTATATCCCTGCGGAGACAGGTAC---AGTTTGGCTGAGTCCAGCTCC 1729
2258 TGACCAAACTATATCCCTGCGGAGACAGGTACAGAAAGTTTGGCTGAGTCCAGCTCC 2317
1730 TCCATGAATCTCAACACCCCGCTGAGATTAACAACAGCTCTCTTCAACGCGACAC 1789
2318 TCCATGAATCTCAACACCCCGCTGAGATTAACAACAGCTCTCTTCAACGCGACAC 2377
1790 ACCCCATGCTGAGCAGGGGCTCTCCGATATGAATCTTCAAGAGACCCCAAAATGGAGTTT 1849
2378 ACCCCATGCTGAGCAGGGGCTCTCCGATATGAATCTTCAAGAGACCCCAAAATGGAGTTT 2437
1850 CCAAGATTAAGTCACTGAGGCAAGCCCTGGGAGAAAGTTGTTTGGGCAATGGATC 1909
2438 CCAAGATTAAGTCACTGAGGCAAGCCCTGGGAGAAAGTTGTTTGGGCAATGGATC 2497
1910 ATGCGGAAGCAGTGGGAATTGACAAAGCAAGCCCAAGAGCGGTCAACCGTGGCGGTG 1969
2498 ATGCGGAAGCAGTGGGAATTGACAAAGCAAGCCCAAGAGCGGTCAACCGTGGCGGTG 2557
1970 AAGATGTTGAAAAGATGATGCCACAGAGAAAGCCTTTCTGATCTGCTGATCAGAGATGAG 2029
2558 AAGATGTTGAAAAGATGATGCCACAGAGAAAGCCTTTCTGATCTGCTGATCAGAGATGAG 2617
2030 ATGATGAAGATGATGAGGAAACAAAGAAATATCATTAATCTTCTGAGAGCTGACACAG 2089
2618 ATGATGAAGATGATGAGGAAACAAAGAAATATCATTAATCTTCTGAGAGCTGACACAG 2677
2090 GATGGGCTCTCTATGTCATAGTGAATGAGCTCTTAAAGGCAACCTCGAAGATACCTC 2149
2678 GATGGGCTCTCTATGTCATAGTGAATGAGCTCTTAAAGGCAACCTCGAAGATACCTC 2737
2150 CGAGCCCGGAGGCCACCCGGGATGAGATCTCTATGATGATTAACCGTGTCTGAGAG 2209
2738 CGAGCCCGGAGGCCACCCGGGATGAGATCTCTATGATGATTAACCGTGTCTGAGAG 2797
2210 CAGATGACCTTCAAGAGCTTGTGTCATGCACTTCCAGCTGAGCCAGACGATGAGATC 2269
2798 CAGATGACCTTCAAGAGCTTGTGTCATGCACTTCCAGCTGAGCCAGACGATGAGATC 2857
2270 TTGGCTTCCCAAAAATGATTCATGAGATTTAGAGCCAGAAATGTTTGGTAAACAGA 2329
2858 TTGGCTTCCCAAAAATGATTCATGAGATTTAGAGCCAGAAATGTTTGGTAAACAGA 2917
2330 AACAAATGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2389
2918 AACAAATGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2977
2390 TACAAATAAACAACAATGAGGAGCTTCCAGTCAAGTGAATGGCTCAGAAACCCGTTT 2449
2978 TACAAATAAACAACAATGAGGAGCTTCCAGTCAAGTGAATGGCTCAGAAACCCGTTT 3037
2450 GATAGATATACATCATCATGAGATGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2509
3038 GATAGATATACATCATCATGAGATGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3097

QY 2510 TTCACTTAGGGGCTGCGCCCTACCCAGGAGATTCGCGTGAAGAACTTTTAAAGCTGCTG 2569
DB 3098 TTCACTTAGGGGCTGCGCCCTACCCAGGAGATTCGCGTGAAGAACTTTTAAAGCTGCTG 3157
QY 2570 AAGGAGAGACAGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2629
DB 3158 AAGGAGAGACAGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3217
QY 2630 AGGAGCTGTTGGCATGCAATGCTCTCCCAAGACCAACCTTCAAGCAGTTGTGTAAGAC 2689
DB 3218 AGGAGCTGTTGGCATGCAATGCTCTCCCAAGACCAACCTTCAAGCAGTTGTGTAAGAC 3277
QY 2690 TTGATGAAATTCACCTCACTCAACCAATGAGAAATTAATGAGCTCAGCAACCTCTC 2749
DB 3278 TTGATGAAATTCACCTCACTCAACCAATGAGAAATTAATGAGCTCAGCAACCTCTC 3337
QY 2750 GAACATATTCACCTCACTCAACCAATGAGAAATTAATGAGCTCAGCAACCTCTC 2809
DB 3338 GAACATATTCACCTCACTCAACCAATGAGAAATTAATGAGCTCAGCAACCTCTC 3397
QY 2810 GTTTTTTCTCAAGACCCCAATGCTTCAAGAACATGCTCTCTCAATCAATCAATCAATCAAT 2869
DB 3398 GTTTTTTCTCAAGACCCCAATGCTTCAAGAACATGCTCTCTCAATCAATCAATCAATCAAT 3457
QY 2870 GGCAGTGTAAACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2929
DB 3458 GGCAGTGTAAACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3517
QY 2930 CCTAGTACACTGACGAGGAGACATGCTCTCCAGAGCTTGTGTCTCACTGTATAT 2989
DB 3518 CCTAGTACACTGACGAGGAGACATGCTCTCCAGAGCTTGTGTCTCACTGTATAT 3577
QY 2990 ATGATCAAGAGATTAATTAATGGAAGAAAGTAAACATATGATGATGATGATGATGATGAT 3048
DB 3578 ATGATCAAGAGATTAATTAATGGAAGAAAGTAAACATATGATGATGATGATGATGATGAT 3636

RESULT 4

US-10-669-920-576
; Sequence 576, Application US/10669920
; Publication No. US20060194265A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
; APPLICANT: Malandro, Marc S.
; TITLE OF INVENTION: NOVEL THERAPEUTIC TARGETS IN CANCER
; FILE REFERENCE: 20366-066001
; CURRENT FILING DATE: US/10/669, 920
; PRIOR FILING DATE: 2003-09-23
; PRIOR APPLICATION NUMBER: US 10/004,113
; PRIOR FILING DATE: 2001-10-23
; PRIOR APPLICATION NUMBER: US 10/052,482
; PRIOR FILING DATE: 2001-11-08
; PRIOR APPLICATION NUMBER: US 09/997,722
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: US 10/034,650
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: US 10/085,117
; PRIOR FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: US 10/087,192
; PRIOR FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 10/322,281
; PRIOR FILING DATE: 2002-12-17
; PRIOR APPLICATION NUMBER: US 10/322,696
; PRIOR FILING DATE: 2002-12-17
; NUMBER OF SEQ ID NOS: 1441
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 576
; LENGTH: 4609
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-669-920-576

Query Match

93.1%; Score 2890.2; DB 6; Length 4609;

Best Local Similarity 97.2%; Pred. No. 0;
Matches 3034; Conservative 0; Mismatches 63; Indels 26; Gaps 8;

QY	1	LCGCGAGCAAAAGTTGGTGGAGGCAAG-CAAAGCTGAGTCTCTTTCTTCTCTCTGTTCC	59
Db	187	CTCCGAGCAAAAGTTGGTGGAGGCAAGCGCAAGCTGAGTCTCTTTCTCTCTCTGTTCC	246
QY	60	CCAAATCCGAGGGGCAAGCCCGGGGGGTATG--GGGTCTCTCGCAGCTCGGGGTACG	116
Db	247	CCAAATCCGAGGGGCAAGCCCGGGGGGTATGTCGCCGCTCTCTCGCAGCTCTGGGGTACG	306
QY	117	GTGAAGCCCGGAGAGCTTGGGCGCGGCGAAGACCCAAAGACCACTCTTCTGCTTGGAG	176
Db	307	GTGAAGCCCGGAGAGCTTGGGCGCGGCGAAGACCCAAAGACCACTCTTCTGCTTGGAG	366
QY	177	TTGCTCCCGCAACCCCGGGGCTCGTGGCTTTCTCATCTCCGACCCAGCGGGGGC-CGGG	235
Db	367	TTGCTCCCGCAACCCCGGGGCTCGTGGCTTTCTCATCTCCGACCCAGCGGGGGCGGGGG	426
QY	236	ACAACAAGGTGCGGAGAGGCGTTGGCAATTCAAGTGACTGACAGAGAGC-GGAGCGCC	294
Db	427	ACAACAAGGTGCGGAGAGGCGTTGGCAATTCAAGTGACTGACAGAGAGCGCGGACGCGC	486
QY	295	TCGGTTCCTGAGCCCAACCGCA-GCTGAAGGCAATTGCGGTAGTCATGCCCCGTAGAAGA	353
Db	487	TCGGTTCCTGAGCCCAACCGGAGGCTGAAGGCAATTGCGGTAGTCATGCCGTAGAAGA	546
QY	354	GTTGTGAGATGGGATTTAAAGTCCACATGGAAGATGTGAAGAAGACCCGGGATTGGTACG	413
Db	547	GTTGTGCAATGGGATTTAAAGTCCACATGGAAGATGTGAAGAAGACCCGGGATTGGTACG	606
QY	414	TAACCATGATGAGCTGGGGTGGTTTCACTGCGTGGTGTGAGTACCAATGGCAACTTGT	473
Db	607	TAACCATGATGAGCTGGGGTGGTTTCACTGCTGGTGTGAGTACCAATGGCAACTTGT	666
QY	474	CCCTGGCCCGGCGCTCTCTTCAAGTTAGTTAGAGATCAACATTAGGCCAGAAAGCCAC	533
Db	667	CCCTGGCCCGGCGCTCTCTTCAAGTTAGTTAGAGATCAACATTAGAGCCAGAAAGCCAC	726
QY	534	CAACCAATTCACCAATCTTCTCAACAGAAAGTGTACTGGCTGGCCAGAGGAGTGGCTAG	593
Db	727	CAACCAATTCACCAATCTTCTCAACAGAAAGTGTACTGGCTGGCCAGAGGAGTGGCTAG	786
QY	594	AGGTGCGTGGCTGTTGAAGAATGCGGCGGATCAGTTGGACTPAAGATGGGGTGCAT	653
Db	787	AGGTGCGTGGCTGTTGAAGAATGCGGCGGATCAGTTGGACTPAAGATGGGGTGCAT	846
QY	654	TGGGCGCCAAACAATAGGACAGTGTCTTATGGGGAGTACTTGCAGATTAAGGGCGCACAC	713
Db	847	TGGGCGCCAAACAATAGGACAGTGTCTTATGGGGAGTACTTGCAGATTAAGGGCGCACAC	906
QY	714	CTAAGACTCCGGGCTCTATGCTTATGCTGACCAAGTAGACGTGTAGACAGTGAACCTTGT	773
Db	907	CTAAGACTCCGGGCTCTATGCTTATGCTGACCAAGTAGACGTGTGAACAGTGAACCTTGT	966
QY	774	ACTTCATGATTAATGTCAAGATGCAATCTCAATCCGAGATGATGAGATGACCCGATG	833
Db	967	ACTTCATGATGATGCAAGATGCAATCTCAATCCGAGATGATGAGATGACCCGATG	1026
QY	834	GTGCGGAAGATTTTGTCAGTAGGAACAGTTAACAAACAAGAGAGCACATATCTGACCAACA	893
Db	1027	GTGCGGAAGATTTTGTCAGTAGGAACAGTTAACAAACAAGAGAGCACATATCTGACCAACA	1086
QY	894	CAGAAAAGATGGAAGAGGGGCTCCATGCTGTGCTCGCGCCACACTGTCAAGTTTCCGT	953
Db	1087	CAGAAAAGATGGAAGAGGGGCTCCATGCTGTGCTCGCGCCACACTGTCAAGTTTCCGT	1146
QY	954	GCCCAAGCCGGGGGAAACCAATGCAACCATGCGGTGGCTGAAGAAACGGGAAGAGGTTTA	1013
Db	1147	GCCCAAGCCGGGGGAAACCAATGCAACCATGCGGTGGCTGAAGAAACGGGAAGAGGTTTA	1206
QY	1014	AGCAGAGCATGCAATTGAGGCTCAAGGTACGAACCAAGCACTGAGGCTCATTTATGG	1073

D	b		1207	AGCAGGACGATCGCATTTGGAGGCTTACAAGTACGAACCAAGACTGGACCTTAATTAG	1268
O	y		1074	AAAGTGTCGCCCATCTGCACAAAGGAAATTATACCTGTGTAGTAGAATGAATACGGGT	1133
D	b		1267	AAAAGTGTGTCCTCATCTGCACAAAGGAAATTATACCTGTGTGTGAGAAATGAATACGGGT	1236
O	y		1134	CCATCATCACAGGTACCCTTGATGTTGTGTGAGCGATCGCTCACCGGCCATCCTCC	1193
D	b		1337	CCATCAATCACACGTACCACTGTGATGTTGTGAGCGCATCGCTCACCGGCCATCCTCC	1386
O	y		1134	AAGCCGACCTGCGCGCAAATGCTCCACAGTGTGTGAGGAGAAGTGAAGTTTGTCTGCA	1253
D	b		1387	AAGCCGACCTGCGCGCAAATGCTCCACAGTGTGTGAGGAGAAGTGAAGTTTGTCTGCA	1446
O	y		1254	AGGTTTACAGTGATGCCCCAGCCCCACATCCAGTGCATCAAGCAGTGGAAAAAGAACGGCA	1313
D	b		1447	AGGTTTACAGTGATGCCCCAGCCCCACATCCAGTGCATCAAGCAGTGGAAAAAGAACGGCA	1506
O	y		1314	GTAATAACGGGCCCCGACGGGCTGCCCTACCTCAAGGTTCTCAGACACTCGGGATTAATA	1373
D	b		1507	GTAATAACGGGCCCCGACGGGCTGCCCTACCTCAAGGTTCTCAGACACTCGGGATTAATA	1566
O	y		1374	GTTCCAAATGCAGAAAGTGTGTGCTGTCTGT-----TCATATGACCGAGCGGATGCTGGGG	1427
D	b		1567	CCACGGACAAAGAAATGAGGATGCTCTATATATTCGAAATGTAACCTTTTGAGACGCTGGGG	1626
O	y		1428	AATATATATGTAAAGTCTCCAATTATATAGGGCAGGCCAACAGTCTGCTGGCTCATG	1487
D	b		1627	AATATATAGTGTGTGGCGGGTAAATCTATATGGGAAATACCTTTTCACTGTGCATGTTGACAG	1686
O	y		1488	TCTCTCCCAAAACAGCAGCGCTTGAGAGAAAGAGATTAACAGCTTCCCACAATACC	1547
D	b		1687	TTCTCTCC-----AGCGCTCGAAGAGAAAGAGATTAACAGCTTCCCACAATACC	1737
O	y		1548	TGGAATATGCCATTATCTGCAATAGGGGTCTCTTAATGCGCTGATATGTTGGTAAACATCA	1607
D	b		1738	TGGAATATGCCATTATCTGCAATAGGGGTCTCTTAATGCGCTGATATGTTGGTAAACATCA	1797
O	y		1608	TCTGTGCGCAATGAAGAACAGACAGCAAGAACCAAGACTTCAGACAGCCGCGCTGTGC	1667
D	b		1788	TCTGTGCGCAATGAAGAACAGACAGCAAGAACCAAGACTTCAGACAGCCGCGCTGTGC	1855
O	y		1668	ACAAGCTGACAAACGATATCCCTCTGCGGAGACAGTTAC---AGTTTGGGCTGAGTCC	1723
D	b		1858	ACAAGCTGACAAACGATATCCCTCTGCGGAGACAGTTAC---AGTTTGGGCTGAGTCC	1917
O	y		1744	AGCTTCTTCATGAATCTCAACAACCCGCTGTGTGAGATTAACAACAACGCTCTCTTCAACG	1783
D	b		1918	AGCTTCTTCATGAATCTCAACAACCCGCTGTGTGAGATTAACAACAACGCTCTCTTCAACG	1977
O	y		1784	GCAGACACCCCACTGTGGCAGGGGTCTCCAGATGAACCTTCAGAGAGACCCAAATATGG	1843
D	b		1978	GCAGACACCCCACTGTGGCAGGGGTCTCCAGATGAACCTTCAGAGAGACCCAAATATGG	2037
O	y		1844	GAGTTTCCAAAGATTAAGCTGACACTGCGCAAGCCCTGGAGAAAGTTGCTTTGGGCAA	1903
D	b		2038	GAGTTTCCAAAGATTAAGCTGACACTGCGCAAGCCCTGGAGAAAGTTGCTTTGGGCAA	2097
O	y		1904	GTTGTTCATGCGGAGAACGATGGAAATTGACAAAGACAGCCCAAGAGACCGGTCAACGCTG	1966
D	b		2098	GTTGTTCATGCGGAGAACGATGGAAATTGACAAAGACAGCCCAAGAGACCGGTCAACGCTG	2157
O	y		1964	GCGGTGAAGATGTTGAAGATGATGCCACAGAGAAAGACTTTTCTGATCTGTGTCAAG	2023
D	b		2158	GCGGTGAAGATGTTGAAGATGATGCCACAGAGAAAGACTTTTCTGATCTGTGTCAAG	2217
O	y		2024	ATGAGATGATGAAGATGATTGGGAAACAAGAATATCATTAATCTTTTGGAGCTTGC	2083
D	b		2218	ATGAGATGATGAAGATGATTGGGAAACAAGAATATCATTAATCTTTTGGAGCTTGC	2277
O	y		2084	ACAACGATGAGGCTCTCTATGTCTATATGATTAATGATGTGCTTAAAGCAACTCCGAGAA	2143
D	b		2278	ACAACGATGAGGCTCTCTATGTCTATATGATTAATGATGTGCTTAAAGCAACTCCGAGAA	2337

2144 TACCTCCGAGCCCGAGGCAACCCCGAGTGAATCTCTTAATGACATTAACTGTTCTT 2203
2338 TACCTCCGAGCCCGAGGCAACCCCGAGTGAATCTCTTAATGACATTAACTGTTCTT 2397
2204 GAGGAGGAGTGAATCTTCAAGGACTTGGTGTCAATGACCTTACAGCTGCGGAGGAGT 2263
2398 GAGGAGGAGTGAATCTTCAAGGACTTGGTGTCAATGACCTTACAGCTGCGGAGGAGT 2457
2264 GAGTACTTGGCTTCCCAAAAATGATATTCATGAGATTAGCAGCAGAAATGTTTGTGA 2323
2458 GAGTACTTGGCTTCCCAAAAATGATATTCATGAGATTAGCAGCAGAAATGTTTGTGA 2517
2324 ACAGAAAAAATGATGATGAAAAATGACAGATTGAGCTTCGCGAGATATCAACATATA 2383
2518 ACAGAAAAAATGATGATGAAAAATGACAGATTGAGCTTCGCGAGATATCAACATATA 2577
2384 GACTATTTACAAAAAACCACCAATGGGCGGCTTCCAGTCAAGTGAATGGCTTCCAGAAC 2443
2578 GACTATTTACAAAAAACCACCAATGGGCGGCTTCCAGTCAAGTGAATGGCTTCCAGAAC 2637
2444 CTGTTGATAGATGATACACTCATGAGTGTCTGGTCTTGGGGGTGTTAATGTGG 2503
2638 CTGTTGATAGATGATACACTCATGAGTGTCTGGTCTTGGGGGTGTTAATGTGG 2697
2504 GAGATCTTCACTTAAAGGGGCTGCGCTTACCCAGGAGATTCCTGTGAGAGAACTTTTAA 2563
2698 GAGATCTTCACTTAAAGGGGCTGCGCTTACCCAGGAGATTCCTGTGAGAGAACTTTTAA 2757
2564 CTGCTGAAGGAGGACACAGATGATGATAGCCAGCACTGACCAAGAACTGATACATG 2623
2758 CTGCTGAAGGAGGACACAGATGATGATAGCCAGCACTGACCAAGAACTGATACATG 2817
2624 ATGATGAGGAGCTGTTGGCATGAGTCCCTCCAGAGACCAACCTTCAAGCATTTGATA 2683
2818 ATGATGAGGAGCTGTTGGCATGAGTCCCTCCAGAGACCAACCTTCAAGCATTTGATA 2877
2684 GAAAGCTTGGATGAAATTTCTCACTCTCACAACCAATGAGAAATCTTGGACCTCAGCCA 2743
2878 GAAAGCTTGGATGAAATTTCTCACTCTCACAACCAATGAGAAATCTTGGACCTCAGCCA 2937
2744 CCTTCGAACAGTATTTCACTGATTAACCTGACACAAAGAAATCTTGGTCTTCAAGAGAT 2803
2938 CCTTCGAACAGTATTTCACTGATTAACCTGACACAAAGAAATCTTGGTCTTCAAGAGAT 2997
2804 GATTCGTTTTTCTCCAGACCCCAATGCTTACAGAACCAATGCTTCTCAGATTCACAC 2863
2998 GATTCGTTTTTCTCCAGACCCCAATGCTTACAGAACCAATGCTTCTCAGATTCACAC 3057
2864 ATAAACGGAGTGTAAACATGATGATGATGCTGTCTGCTGTCCCAACAGAGACAGC 2923
3058 ATAAACGGAGTGTAAACATGATGATGATGCTGTCTGCTGTCCCAACAGAGACAGC 3117
2924 TGGGAACCTAGCTACCTAGACAGGAGAACATGCTTCCAGAGCTGTTGTTCTCCACT 2983
3118 TGGGAACCTAGCTACCTAGACAGGAGAACATGCTTCCAGAGCTGTTGTTCTCCACT 3177
2984 GATATATGATCAGAGAGTAAATATGAAAAATGAAATATGATGATGATGATGATGAT 3043
3178 GATATATGATCAGAGAGTAAATATGAAAAATGAAATATGATGATGATGATGATGAT 3237
3044 ATACAGTTGAAAACTTGTATCTTCCAGAGAGAGAAAGGTTTCTGAGCAAGTGCAC 3103
3238 ATACAGTTGAAAACTTGTATCTTCCAGAGAGAGAAAGGTTTCTGAGCAAGTGCAC 3297
3104 TGC 3106
3298 TGC 3300

RESULT 5

US-10-669-920-564
; Sequence 564, Application US/10669920

Publication No. US20060194265A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
; APPLICANT: Malandro, Marc S.
; TITLE OF INVENTION: NOVEL THERAPEUTIC TARGETS IN CANCER
; FILE REFERENCE: 20366-066001
; CURRENT APPLICATION NUMBER: US/10/669,920
; CURRENT FILING DATE: 2003-09-23
; PRIOR APPLICATION NUMBER: US 10/004,113
; PRIOR FILING DATE: 2001-10-23
; PRIOR APPLICATION NUMBER: US 10/052,482
; PRIOR FILING DATE: 2001-11-08
; PRIOR APPLICATION NUMBER: US 09/997,722
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: US 10/034,650
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: US 10/085,117
; PRIOR FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: US 10/087,192
; PRIOR FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 10/322,281
; PRIOR FILING DATE: 2002-12-17
; PRIOR APPLICATION NUMBER: US 10/322,696
; PRIOR FILING DATE: 2002-12-17
; NUMBER OF SEQ ID NOS: 1441
; SOFTWARE: PastSeq for Windows Version 4.0
; SEQ ID NO 564
; LENGTH: 5000
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-669-920-564

Query Match 93.1%; Score 2890.2; DB 6; Length 5000;
Best Local Similarity 97.2%; Pred. No. 0;
Matches 3034; Conservative 0; Mismatches 63; Indels 26; Gaps 8;
QY 1 CCGCGAGCAAGTTGGTGAAGGCAACG-CAGCGTAGTCTTTCTTCTCTGTTCC 59
DB 578 CTGCGAGCAAGTTGGTGAAGGCAACGCAAGCTGATGCTTTCTTCTCTGTTCC 637
QY 60 CCAATCCGAGGAGCGCCGCGGCGTCAATG---GCGCTCTCCGAGCCTGGGATACGC 116
DB 638 CCAATCCGAGGAGCGCCGCGGCGTCAATG---GCGCTCTCCGAGCCTGGGATACGC 697
QY 117 GTAAAGCCCGGAGGCTTGGCGCGGAGAAACCAAGAACCACTTTCTGCTTTGAG 176
DB 698 GTAAAGCCCGGAGGCTTGGCGCGGAGAAACCAAGAACCACTTTCTGCTTTGAG 757
QY 177 TTGCTCCCGGACCCCGGCGTGTGCTTCTTCATCCGACCAAGCGGGGC-CGGGG 235
DB 758 TTGCTCCCGGACCCCGGCGTGTGCTTCTTCATCCGACCAAGCGGGGC-CGGGG 817
QY 236 ACAACACAGTTCGCGAGAGAGCTTGCATTCAGATGACCTGACAGAGCAGC-GCAGCGC 294
DB 818 ACAACACAGTTCGCGAGAGAGCTTGCATTCAGATGACCTGACAGAGCAGCAGC 877
QY 295 TCGGTTCTGAGCCCAACCGCA-GCTGAAGGATTCGCGGTGTCTCATTCCTGTAGAGAA 353
DB 878 TCGGTTCTGAGCCCAACCGCAGCGCTGAAGGATTCGCGGTGTCTCATTCCTGTAGAGAA 937
QY 354 GTGTCAGATGGAGTTAATGATCAATGAGATGAGAAAGAGACCGGGGATTTGGTACCG 413
DB 938 GTGTCAGATGGAGTTAATGATCAATGAGATGAGAAAGAGACCGGGGATTTGGTACCG 997
QY 414 TAACATGATGATGAGGCTGCTTCACTGATGATGATGATGATGATGATGATGATGATGAT 473
DB 998 TAACATGATGATGAGGCTGCTTCACTGATGATGATGATGATGATGATGATGATGATGAT 1057
QY 474 CCTGGCCCGGCGCTCTTCACTGATGATGATGATGATGATGATGATGATGATGATGATGAT 533
DB 1058 CCTGGCCCGGCGCTCTTCACTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1117
QY 534 CAACCAATACCAATCTCTCAACCAAGATGATGATGATGATGATGATGATGATGATGATGAT 593

Db	1118	CAACCAATYACCAAAATCTCTCAACCAAGATGTAGTGGCTGCGCAAGGGAATGCTGCTAG	11777
OY	594	AGGTGCGCTGCTGTGTGAAGAATGCGCGCGTGAATCA GTTGA CTAAAGATGGGGTGC ACT	653
Db	1178	AGGTGCGCTGCTGTGTGAAGAATGCGCGCGTGAATCA GTTGA CTAAAGATGGGGTGC ACT	1237
OY	654	TGGGCGCCCAACATATAGGACAGTGTCTTATTTGGGAGTACTTTCAGATTAAGGCGCCGACAC	713
Db	1238	TGGGCGCCCAACATATAGGACAGTGTCTTATTTGGGAGTACTTTCAGATTAAGGCGCCGACAC	1297
OY	714	CTAGAGACTCCGGCTCTTATGTCTTACTGTCACTAGAGACTGTAGACAGTGAACCTTGGT	773
Db	1298	CTAGAGACTCCGGCTCTTATGTCTTACTGTCACTAGAGACTGTAGACAGTGAACCTTGGT	1357
OY	774	ACTTCATGTGAATGTCA CAGATGCATCTCA TCCGAGATGATGAGATGACCCGATG	833
Db	1358	ACTTCATGTGAATGTCA CAGATGCATCTCA TCCGAGATGATGAGATGACCCGATG	1417
OY	834	GTGCGGAAGATTTTGTCA GTAGAACAGTAA CAA CAAAGAGACCATATCTGACCAACA	893
Db	1418	GTGCGGAAGATTTTGTCA GTAGAACAGTAA CAA CAAAGAGACCATATCTGACCAACA	1477
OY	894	CAGAAAAGATGAAAAAGCGGCTCCATGCTGTGCTCTGGGCCCAACTGTCAAGTTTGGCT	953
Db	1478	CAGAAAAGATGAAAAAGCGGCTCCATGCTGTGCTCTGGGCCCAACTGTCAAGTTTGGCT	1537
OY	954	GCCCAAGCGGGGGGGAACCCAAATGCCAACATAGCGGTGCTGAAAAAGGGAAGGTTTA	1013
Db	1538	GCCCAAGCGGGGGGGAACCCAAATGCCAACATAGCGGTGCTGAAAAAGGGAAGGTTTA	1597
OY	1014	AGCAGGACATCGCA TTTGGAAGGCTTCAAGATACGAAC CAGCACTGAGCCTCA TTTATG	1073
Db	1598	AGCAGGACATCGCA TTTGGAAGGCTTCAAGATACGAAC CAGCACTGAGCCTCA TTTATG	1657
OY	1074	AAAGTGTGTCCTCATCTGA CAAAGGAAATTATCCTGTGTAGTGAATGAATACGGGT	1133
Db	1658	AAAGTGTGTCCTCATCTGA CAAAGGAAATTATCCTGTGTAGTGAATGAATACGGGT	1717
OY	1134	CCATCAATCA CACGTACCA CCGTAGATGTTGTGAGACGATTCGCTCACCGGCCCATCCCTC	1199
Db	1718	CCATCAATCA CACGTACCA CCGTAGATGTTGTGAGACGATTCGCTCACCGGCCCATCCCTC	1777
OY	1194	AAGCCGAGCTCCCGGCAATGCTCTCA CAGTGTGTGAGAGAGCTGAAGTGTGTCTGCA	1253
Db	1778	AAGCCGAGCTCCCGGCAATGCTCTCA CAGTGTGTGAGAGAGCTGAAGTGTGTCTGCA	1837
OY	1254	AGGTTTACATGATGATGCCAGGCCCACTCCAGTGTATCAAGCAGCTGGA AAAAGACGCA	1313
Db	1838	AGGTTTACATGATGATGCCAGGCCCACTCCAGTGTATCAAGCAGCTGGA AAAAGACGCA	1897
OY	1314	GTAATTAACGGGCCCCGAGCGGCTGCCCTTACCTCAAGGTTCTGAAGCACTCCGGGTAATA	1373
Db	1898	GTAATTAACGGGCCCCGAGCGGCTGCCCTTACCTCAAGGTTCTGAAGCACTCCGGGTAATA	1957
OY	1374	GTTCCATATGCAAGATGTGCTGCTGTGT-----TCAATGTGACGAGCGGATGCTGGGG	1427
Db	1958	CCACGGA CAAAGAGATTGAAGTTCTCTATATTCCGAAATGTAACTTTTGAAGACGTGGGG	2017
OY	1428	AATATATATGTAAAGGTTCTCAATTTATTAAGGCAAGCCACCAAGCTTGCTGCTCACTG	1487
Db	2018	AATATATGTCGTGCGGGTAAATTTCTAATGGGATATCTTTCACTCTGCAATGTGTGACAG	2077
OY	1488	TCCTGCCCAAAACAGCAGCGCTGTGAAGAGAAAAGAGATTACAGCTTCCCAAGCTAAC	1547
Db	2078	TCCTGCCCAAAACAGCAGCGCTGTGAAGAGAAAAGAGATTACAGCTTCCCAAGCTAAC	2128
OY	1548	TGAGATATGCACTTACTGATCATAGGGGCTTCTTATAGCCTGTATGTGTGTTA CAGTCA	1607
Db	2129	TGAGATATGCACTTACTGATCATAGGGGCTTCTTATAGCCTGTATGTGTGTTA CAGTCA	2188
OY	1608	TCCTGTGCGGAATGAAGACAGCACAAGAACGACCTTCAGACGCAAGCGGCTGTGCTC	1667

Dd	2189	TTCTGTGCCAATTAAGAACACGACCAAGAAAGCCAGCTTCAGCAGGCGAGCGGCTGTGC	2248
Qy	1668	ACAAGCTGACCAAAAGTATCCCTCGCGAGACAGGTAAAC---AGTTTGGCTGAATCC	1723
Dd	2249	ACAAGCTGACCAAAAGTATCCCTCGCGAGACAGGTAAACAGAAAGTTTGGCTGAATCC	2308
Qy	1724	AGCTTCCTCATGAACTCCAAACACCCCGCTGTGTGGATTAACAAGCCTCTCTTAACG	1783
Dd	2309	AGCTTCCTCATGAAGCTCCAAACACCCCGCTGTGTGGATTAACAAGCCTCTCTTAACG	2368
Qy	1784	GCAGACACCCCATGCTGGCAGGGGTCTCCAGATATACTTCAGAGGACCCAAAATGG	1843
Dd	2389	GCAGACACCCCATGCTGGCAGGGGTCTCCAGATATACTTCAGAGGACCCAAAATGG	2428
Qy	1844	GAGTTTCCAAAGATAAGCTGACACTGAGGACAGCCCTGGAGAGAGGTGTCTTTGGCCAA	1903
Dd	2429	GAGTTTCCAAAGATAAGCTGACACTGAGGACAGCCCTGGAGAGAGGTGTCTTTGGCCAA	2488
Qy	1904	GTGCTCATGTGGGGAAGCAGTGGGAATTGACAAACAAAGCCCAAGAGGGGTGACCGGTG	1963
Dd	2489	GTGCTCATGTGGGGAAGCAGTGGGAATTGACAAACAAAGCCCAAGAGGGGTGACCGGTG	2548
Qy	1964	GCCTGTAAGATGTGAAGAATGATGACCAAGAGAAAGACCTTTCTGATCTGTGTCAAG	2023
Dd	2549	GCCTGTAAGATGTGAAGAATGATGACCAAGAGAAAGACCTTTCTGATCTGTGTCAAG	2608
Qy	2024	ATGAGATGATGAAGATGATTTGGGAAAACAAGATATCATAAATCTTCTTGAAGCTGC	2083
Dd	2609	ATGAGATGATGAAGATGATTTGGGAAAACAAGATATCATAAATCTTCTTGAAGCTGC	2668
Qy	2084	ACAACAGATGGGCTCTCTATGTCAATGTTGAGTATGCTCTTAAAGCACTCCGAGAA	2143
Dd	2669	ACAACAGATGGGCTCTCTATGTCAATGTTGAGTATGCTCTTAAAGCACTCCGAGAA	2728
Qy	2144	TACCTCCGAGCGGGAAGGCCACCGGGATGGAAGTACTCTATGACATTAACCGGTTCCT	2203
Dd	2729	TACCTCCGAGCGGGAAGGCCACCGGGATGGAAGTACTCTATGACATTAACCGGTTCCT	2788
Qy	2204	GAGAGCAGATGACCTTCAAGACCTTGATGTCAATGACCTTACAGCTGGCCAGACGATG	2263
Dd	2789	GAGAGCAGATGACCTTCAAGACCTTGATGTCAATGACCTTACAGCTGGCCAGACGATG	2848
Qy	2264	GAGTACTTGGCTCCAAAAATGTATTCACTGAGATTTAGCAGCCAGAAATGTTTGGTA	2323
Dd	2849	GAGTACTTGGCTCCAAAAATGTATTCACTGAGATTTAGCAGCCAGAAATGTTTGGTA	2908
Qy	2324	ACAAGAAAACAATGATGAAGAAATGACGACTTTGSCATCCGACAGATATCAACAATA	2383
Dd	2909	ACAAGAAAACAATGATGAAGAAATGACGACTTTGSCATCCGACAGATATCAACAATA	2968
Qy	2384	GACTATTACAAAAAGACCAACCAATGGGCGGCTTCAGTCAAGTGAATGCTCCAGAAAGC	2443
Dd	2969	GACTATTACAAAAAGACCAACCAATGGGCGGCTTCAGTCAAGTGAATGCTCCAGAAAGC	3028
Qy	2444	CTGTTTGAATAGTATACACTCATCAAGATGATGTGTGTCCTTCGAGGTGTAAATGTGG	2503
Dd	3029	CTGTTTGAATAGTATACACTCATCAAGATGATGTGTGTCCTTCGAGGTGTAAATGTGG	3088
Qy	2504	GAGATCTTCACTTTAAGGGGGCTCGCCCTTACCAGAGGATTCGCCGTGGAGGAACCTTTTAAAG	2563
Dd	3089	GAGATCTTCACTTTAAGGGGGCTCGCCCTTACCAGAGGATTCGCCGTGGAGGAACCTTTTAAAG	3148
Qy	2564	CTGCTGAAGGAAGACACAGATGGAATTAAGCCAGCCCAACTGACCAAGAACTGTACATG	2623
Dd	3149	CTGCTGAAGGAAGACACAGATGGAATTAAGCCAGCCCAACTGACCAAGAACTGTACATG	3208
Qy	2624	ATGATGAAGGACTGTGTGCATGCAATGTCCTCCCAAGACCAACGTTCAAGCAATTGGTA	2683
Dd	3209	ATGATGAAGGACTGTGTGCATGCAATGTCCTCCCAAGACCAACGTTCAAGCAATTGGTA	3268
Qy	2684	GAAGACTTGGATCGAATTTCTCACTCTCAACCAATAGAGAAATCTTGGACTTCAGCCAA	2743
Dd	3269	GAAGACTTGGATCGAATTTCTCACTCTCAACCAATAGAGAAATCTTGGACTTCAGCCAA	3328

QY	2744	CCCTCTCGAACAGTATTCACCTAGTAAACCTCGACACAAAGATCTTGTTCTTCAGGAGAT	2803
Db	3329	CCCTCTCGAACAGTATTCACCTAGTAAACCTCGACACAAAGATCTTGTTCTTCAGGAGAT	3388
QY	2804	GATTCTGTGTTTTCTTCAGACCCCATGCGCTTACGAAACCATGCTCTCCAGTATTCACAC	2863
Db	3389	GATTCTGTGTTTTCTTCAGACCCCATGCGCTTACGAAACCATGCTCTCTCCAGTATTCACAC	3448
QY	2864	ATPAAACGGCAGTGTAAAAACATGAATGACTGTGTGCTGTGCCCTGTCCCAACACGACACAC	2923
Db	3449	ATPAAACGGCAGTGTAAAAACATGAATGACTGTGTGTGCTGTGCCCTGTCCCAACACGACACAC	3508
QY	2924	TGGGAACTTACTCTACATCGACACGAGGAACCATGCGTCCCGAGGCTGTGTCTCCACTT	2983
Db	3509	TGGGAACTTACTCTACATCGACACGAGGAACCATGCGTCCCGAGGCTGTGTCTCCACTT	3568
QY	2984	GTAATATATGATCAGAGGAGTAAATAAATTGGAAAGATATACGATATGTGTAAAGATT	3043
Db	3569	GTAATATATGATCAGAGGAGTAAATAAATTGGAAAGATATACGATATGTGTAAAGATT	3628
QY	3044	ATPACGTTGAAAACTTGTATCTTCCCAAGAGGAAAGAAAGTCTTCGAGACAGTGCAC	3103
Db	3629	ATPACGTTGAAAACTTGTATCTTCCCAAGAGGAAAGAAAGTCTTCGAGACAGTGCAC	3688
QY	3104	TGC 3106	
Db	3689	TGC 3691	

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RESULT 6
US-10-669-920-634
? Sequence 634, Application US/10669920
? Publication No. US20060194265A1
? GENERAL INFORMATION:
? APPLICANT: Malandro, Marc S.
? APPLICANT: Morris, David W.
? TITLE OF INVENTION: NOVEL THERAPEUTIC TARGETS IN CANCER
? FILE REFERENCE: 20366-066001
? CURRENT APPLICATION NUMBER: US/10/669,920
? CURRENT FILING DATE: 2003-09-23
? PRIOR APPLICATION NUMBER: US 10/004,113
? PRIOR FILING DATE: 2001-10-23
? PRIOR APPLICATION NUMBER: US 10/052,482
? PRIOR FILING DATE: 2001-11-08
? PRIOR APPLICATION NUMBER: US 09/997,722
? PRIOR FILING DATE: 2001-11-30
? PRIOR APPLICATION NUMBER: US 10/034,650
? PRIOR FILING DATE: 2001-12-20
? PRIOR APPLICATION NUMBER: US 10/085,117
? PRIOR FILING DATE: 2002-02-27
? PRIOR APPLICATION NUMBER: US 10/087,192
? PRIOR FILING DATE: 2002-03-01
? PRIOR APPLICATION NUMBER: US 10/322,281
? PRIOR FILING DATE: 2002-12-17
? PRIOR APPLICATION NUMBER: US 10/322,696
? PRIOR FILING DATE: 2002-12-17
? NUMBER OF SEQ ID NOS: 1441
? SOFTWARE: PatSeq for Windows Version 4.0
? SEQ ID NO 634
? LENGTH: 4990
? TYPE: DNA
? ORGANISM: Homo sapiens
US-10-669-920-634

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Query Match	92.8%	Score 2882.2;	DB 6;	Length 4990;
Best Local Similarity	97.1%	Pred. No. 0;		
Matches 3028; Conservative	0;	Mismatches 63;	Indels 28;	Gaps 8;

QY 1 CCGCGAGCAAAAGTTTGATGTGAGGCGCAAG-CAAGCTGAGTCTTTCTTCTCTGCTTC 59
Db 578 CTGCGAGCAAAAGTTTGATGTGAGGCGCAAGCTGAGTCTTTCTTCTCTGCTTC 637

QY	60	CCAAATCCGAGGGGAGGCGCGGGGCGTCATG---GGGCTCTCCGACGCTGGGGTACGC	116
Db	638	CCAAATCCGAGGGGAGGCGCGGGGCGTCATGCGCGCTCTCTCCGACGCTGGGGTACGC	697
QY	117	GTGAAGCCCGGGAGGAGCTTGGCGCGCGGGAGAGACCACAGACCACTCTTCTGCGTTTGGAG	176
Db	698	GTGAAGCCCGGGAGGAGCTTGGCGCGCGGGAGAGACCACAGACCACTCTTCTGCGTTTGGAG	757
QY	177	TTTGCTCCCGCAACCCCGGCGTCTGCTCTTTCATATCCGACCCACGCGGGGC--CGGGG	235
Db	758	TTTGCTCCCGCAACCCCGGCGTCTGCTCTTTCATATCCGACCCACGCGGGGCGCGGGG	817
QY	236	ACAAACACAGGTCGCGGAGAGCGCTTGCCATTCAAATGACATGACAGCAGCAGC--GCAGCGCC	294
Db	818	ACAAACACAGGTCGCGGAGAGCGCTTGCCATTCAAATGACATGACAGCAGCAGCAGCGCC	877
QY	295	TGCGTTCTGAGCCACCGCA--GCTGAAGGCAATTGCGCGTAGTCATGCCCCGTAGAGGAA	353
Db	878	TGCGTTCTGAGCCACCGCAAGCGTGGAAGCAATTCGCGTAGTCATGCCCCGTAGAGGAA	937
QY	354	GTGTGCAGANTGGATTAACTGTCAATGAGAGATATGGAAGAGACCGGGGATTGTATCG	413
Db	938	GTGTGCAGANTGGATTAACTGTCCAATGAGAGATATGGAAGAGACCGGGGATTGTATCG	997
QY	414	TAAACATGTCAGCTGGGGGTGTTTCATCTGCGTGTGTGTGTATCCATGGCAACTTTGT	473
Db	998	TAAACATGTCAGCTGGGGGTGTTTCATCTGCGTGTGTGTGTATCCATGGCAACTTTGT	1057
QY	474	CCCTGAGCCGGGCGCTCTCTTCAGTTATGTTAGATATACCAATTGAGCCAGAAAGCAC	533

QY	534	CAACCAATATCCAAATCTCTCAACCAAGATGTCGTGGCTGCAGAGGGAGTCGTAG	593
Db	1118	CACCAATATCCAAATCTCTCAACCAAGATGTCGTGGCTGCAGAGGGAGTCGTAG	1177
QY	554	AGGTGCGCTGCTGTTGAAAGATGCGCGCGTATCATTTGGACTTAAGATGGGGTGCACT	653
Db	1178	AGGTGCGCTGCTGTTGAAAGATGCGCGCGTATCATTTGGACTTAAGATGGGGTGCACT	123
QY	654	TGGGGCCCAACAATGAGCAGTGTCTTATGGGGAGTACTTCAGATTAAGGGCCGCAAC	713
Db	1238	TGGGGCCCAACAATGAGCAGTGTCTTATGGGGAGTACTTCAGATTAAGGGCCGCAAC	1297
QY	714	CTAGAGACTCGGCGCTTATGCTTGTACTGCCAGTAGAGCTGTAGACATGTAACTTGGT	773
Db	1298	CTAGAGACTCGGCGCTTATGCTTGTACTGCCAGTAGAGCTGTAGACATGTAACTTGGT	1357
QY	774	ACTTCATGTTGATGTCACAGTGGCACTCTCATCCGAGATGATAGATGACCCGATG	833
Db	1358	ACTTCATGTTGATGTCACAGTGGCACTCTCATCCGAGATGATAGATGACCCGATG	1417
QY	834	GTGCGGAAGATTTTGTCAATGAGAACAGTAAACAACAAGAGCACCATTACTGGACCAACA	893
Db	1418	GTGCGGAAGATTTTGTCAATGAGAACAGTAAACAACAAGAGCACCATTACTGGACCAACA	1477
QY	894	CAGAAAAAGTGGAAAAAGCGCTCCATGCTGTGCCGCGGCCCAACCTGTCAAGTTTCGT	953
Db	1478	CAGAAAAAGTGGAAAAAGCGCTCCATGCTGTGCCGCGGCCCAACCTGTCAAGTTTCGT	1537
QY	954	GCCCAAGCCGGGGGAAACCAATGCAACCATGCGGTGGCTGTAAGAAACGGGAAGAGTTTA	1013
Db	1538	GCCCAAGCCGGGGGAAACCAATGCAACCATGCGGTGGCTGTAAGAAACGGGAAGAGTTTA	1597
QY	1014	AGCAGAGCATTTGCAATTGGAGGCTTCAAGGTTCAGAAACAGACTTGGAGCCCTATTATGG	1073
Db	1598	AGCAGAGCATTTGCAATTGGAGGCTTCAAGGTTCAGAAACAGACTTGGAGCCCTATTATGG	1657
QY	1074	AAAGTGTGTCCTCATCTGCAAGAGGAAATTATACCTGTGTATGTGAGATGAATACGGGT	1133
Db	1658	AAAGTGTGTCCTCATCTGCAAGAGGAAATTATACCTGTGTGTGAGATGAATACGGGT	1717
QY	1134	CCATCATGCAACGTAACAACCTGAGTGTGTGGAGCGATGCGCTTACCGGCCCATCTTCC	1197

DB 1718 CCATCATATACAGTACACCTGATGTTGTGTGAGAGGATCGCTCCACCGGCACTCTCC 1777
QY 1194 AAGCCGAGCTGCGCGCAAAATGCTCTCAACAGTGTGAGAGAGAGCTAGAGTTGTCTGCA 1253
DB 1778 AAGCCGAGCTGCGCGCAAAATGCTCTCAACAGTGTGAGAGAGAGCTAGAGTTGTCTGCA 1837
QY 1254 AGGTTTACAGTATGCTCCAGCCCAATCATGATGATCAAGCACTGTGAGAAAGAGGCA 1313
DB 1838 AGGTTTACAGTATGCTCCAGCCCAATCATGATGATCAAGCACTGTGAGAAAGAGGCA 1897
QY 1314 GTAATATACGAGCCGAGCGGCTGCTCACTCAAGGTTCTCAAGCACTGCGGGATTAATA 1373
DB 1898 GTAAATACGAGCCGAGCGGCTGCTCACTCAAGGTTCTCAAGCGCGCGGTTTAA 1957
QY 1374 GTTCCAGTACAGAGTGTGCTGTGT-----TCAATGTGACCAAGCGGATGCTGGG 1427
DB 1958 CCAAGGACAAAGAGATTAAGGTTCTCTATATTCGAATGTAATCTTTTGAAGAGCTGGG 2017
QY 1428 AATATATATGTAAGTGTCTCAATTAATATAGGAGAGGCAACAGTGTGCTGCTCACTG 1487
DB 2018 AATATATGCTGTGGGATTAATCTATGGAATATCTTTCATCTGATGATGTTGACG 2077
QY 1488 TCTTCGCAAAACAGCAAGCGCTGGAAGAGAAAGAGATTAAGGTTCCCGGAGCTACG 1547
DB 2078 TTTCTGCT-----AGCGCTGGAAGAGAAAGAGATTAAGGTTCCCGGAGCTACG 2128
QY 1548 TGAAGATACCATTTATCTGATAGGAGTCTTCTTAAATGCTGTATGATGTAACAGTCA 1607
DB 2129 TGAAGATACCATTTATCTGATAGGAGTCTTCTTAAATGCTGTATGATGTAACAGTCA 2188
QY 1608 TCTGTGCGGATGAGAAACAGCAACAGCACTTCAAGAGCCAGCGGCTGTG 1667
DB 2189 TCTGTGCGGATGAGAAACAGCAACAGCACTTCAAGAGCCAGCGGCTGTG 2248
QY 1668 ACAAGCTGACCAACGATCTCCCTGCGGAGACAGGTTAAGTTGCGCTGAGTCCAGCT 1727
DB 2249 ACAAGCTGACCAACGATCTCCCTGCGGAGACG-----GTTTGGCTGAGTCCAGCT 2302
QY 1728 CTTCCATGAACTTCCACACCGCGCTGTGAGATTAACACAGCTCTCTTCAACGCGCAG 1787
DB 2303 CTTCCATGAACTTCCACACCGCGCTGTGAGATTAACACAGCTCTCTTCAACGCGCAG 2362
QY 1788 ACAACCCCATGCTGCGAGGAGTCTCCGATATGAATCTTCAAGAGACCCAAAATGGAGT 1847
DB 2363 ACAACCCCATGCTGCGAGGAGTCTCCGATATGAATCTTCAAGAGACCCAAAATGGAGT 2422
QY 1848 TTTCCAGAGATTAAGTGAACCTGCGGAGACCGCTGCGGAGAGGTTGCTTGGCAAGTGG 1907
DB 2423 TTTCCAGAGATTAAGTGAACCTGCGGAGACCGCTGCGGAGAGGTTGCTTGGCAAGTGG 2482
QY 1908 TCAATGCGAGAGAGTGGAGATTGAACAAGACCAAGAGAGCGGTCAACGTTGGCG 1967
DB 2483 TCAATGCGAGAGAGTGGAGATTGAACAAGACCAAGAGAGCGGTCAACGTTGGCG 2542
QY 1968 TGAAGATGTTGAAGATGATGCAACAGAGAAAGCTTTCTGATCTGTGTGAGATGG 2027
DB 2543 TGAAGATGTTGAAGATGATGCAACAGAGAAAGCTTTCTGATCTGTGTGAGATGG 2602
QY 2028 AGATGATGAAGATTTGGGAAACACAAGATATCAATTAATCTTGGAGCTGCAAC 2087
DB 2603 AGATGATGAAGATTTGGGAAACACAAGATATCAATTAATCTTGGAGCTGCAAC 2662
QY 2088 AGATGAGGCTCTCTATGTCATAGTATGATGCTCTTAAGGCAACCTCCGAGATAC 2147
DB 2663 AGATGAGGCTCTCTATGTCATAGTATGATGCTCTTAAGGCAACCTCCGAGATAC 2722
QY 2148 TCCGAGCCGAGAGCCACCCGAGATGAGTATCTCTATGATCAATTAACGTTTCTGAG 2207
DB 2723 TCCGAGCCGAGAGCCACCCGAGATGAGTATCTCTATGATCAATTAACGTTTCTGAG 2782
QY 2208 AGCAGATGACCTTCAAGACTTGTGTGATGATCACTACGAGCTGCGCAAGCGAGT 2267

DB 2783 AGCAGATGACCTTCAAGACTTGTGTGATGATGATCACTACCAAGCTGCGCAAGGATGAGT 2842
QY 2268 ACTTGGCTTCCCAAAATGATTAATTCAGATTTATGAGCCAGAAATGTTTGTAAAG 2327
DB 2843 ACTTGGCTTCCCAAAATGATTAATTCAGATTTATGAGCCAGAAATGTTTGTAAAG 2902
QY 2328 AAAACAGTGTATGAAAATGAGAGCTTGTGATGCTGCGCAGAGATTAACAATATAGACT 2387
DB 2903 AAAACAGTGTATGAAAATGAGAGCTTGTGATGCTGCGCAGAGATTAACAATATAGACT 2962
QY 2388 ATTAACAAAAGACCAACAAATGAGCGGCTTCAAGTCAAGTATGCTCAAGAACCTGT 2447
DB 2963 ATTAACAAAAGACCAACAAATGAGCGGCTTCAAGTCAAGTATGCTCAAGAACCTGT 3022
QY 2448 TTGATGATGATTAACCTCATGAGTATGATGATGATGATGATGATGATGATGATGAT 2507
DB 3023 TTGATGATGATTAACCTCATGAGTATGATGATGATGATGATGATGATGATGATGAT 3082
QY 2508 TCTTCACTTATGAGGAGCTGCGCTCAACCGAGGATTCGCTGAGAGAACTTTTAAAGCTG 2567
DB 3083 TCTTCACTTATGAGGAGCTGCGCTCAACCGAGGATTCGCTGAGAGAACTTTTAAAGCTG 3142
QY 2568 TGAAGAGAGACACAGATGATTAAGCCAGCACTGACCAAGAACTGTACATGATGA 2627
DB 3143 TGAAGAGAGACACAGATGATTAAGCCAGCACTGACCAAGAACTGTACATGATGA 3202
QY 2628 TGAAGAGCTGTTGGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2687
DB 3203 TGAAGAGCTGTTGGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3262
QY 2688 ACTTGGATGATTTCTCATCTTCAACCAAGAGATTAAGTGTGAGCTCAAGCACTG 2747
DB 3263 ACTTGGATGATTTCTCATCTTCAACCAAGAGATTAAGTGTGAGCTCAAGCACTG 3322
QY 2748 TGAACAGATTAACCTTACCTTGAACAAAGATTTCTTGTCTTGAAGATGAT 2807
DB 3323 TGAACAGATTAACCTTACCTTGAACAAAGATTTCTTGTCTTGAAGATGAT 3382
QY 2808 CTGTTTTTCTCAGACCCCATGCTTACAGACCAATGATGATGATGATGATGATGAT 2867
DB 3383 CTGTTTTTCTCAGACCCCATGCTTACAGACCAATGATGATGATGATGATGATGAT 3442
QY 2868 AGGAGAGTGAACATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2927
DB 3443 AGGAGAGTGAACATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3502
QY 2928 AACCTAGTACACTGAGAGAGACCAATGCTTCCAGAGCTTGTGTCTCACTGTAT 2987
DB 3503 AACCTAGTACACTGAGAGAGACCAATGCTTCCAGAGCTTGTGTCTCACTGTAT 3562
QY 2988 ATATGATCAGAGAGTAAATTAATGAAAAGTATCAGCATATGTTAAAGTTATAC 3047
DB 3563 ATATGATCAGAGAGTAAATTAATGAAAAGTATCAGCATATGTTAAAGTTATAC 3622
QY 3048 AGTTGAAAACCTGTATCTTCCCGAGAGAGAAAGGTTTCTGAGAGTGAAGCTGC 3106
DB 3623 AGTTGAAAACCTGTATCTTCCCGAGAGAGAAAGGTTTCTGAGAGTGAAGCTGC 3681

RESULT 7
US-10-669-920-608
; Sequence 608, Application US/10669920
; Publication No. US20060194265A1
; GENERAL INFORMATION:
; APPLICANT: Moris, David W.
; APPLICANT: Malandro, Marc S.
; TITLE OF INVENTION: NOVEL THERAPEUTIC TARGETS IN CANCER
; FILE REFERENCE: 20366-066001
; CURRENT APPLICATION NUMBER: US/10/669,920
; PRIOR FILING DATE: 2003-09-23
; PRIOR APPLICATION NUMBER: US 10/004,113
; PRIOR FILING DATE: 2001-10-23
; PRIOR APPLICATION NUMBER: US 10/052,482

PRIOR FILING DATE: 2001-11-08
PRIOR APPLICATION NUMBER: US 09/997,722
PRIOR FILING DATE: 2001-11-30
PRIOR APPLICATION NUMBER: US 10/034,650
PRIOR FILING DATE: 2001-12-20
PRIOR APPLICATION NUMBER: US 10/085,117
PRIOR FILING DATE: 2002-02-27
PRIOR APPLICATION NUMBER: US 10/087,192
PRIOR FILING DATE: 2002-03-01
PRIOR APPLICATION NUMBER: US 10/322,281
PRIOR FILING DATE: 2002-12-17
PRIOR APPLICATION NUMBER: US 10/322,696
PRIOR FILING DATE: 2002-12-17
NUMBER OF SEQ ID NOS: 1441
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 608
LENGTH: 4607
TYPE: DNA
ORGANISM: Homo sapiens
US-10-669-920-608

Query Match 92.3%; Score 2867.8; DB 6; Length 4607;

Best Local Similarity 96.7%; Pred. No. 0;
Matches 3024; Conservative 0; Mismatches 67; Indels 36; Gaps 8;

QY 1 CCCGAGCAAAATTGTTGAGGCAACG-CAAGCTGATCTTTCTCTCTCTCC 59
DB CTGCGAGCAAAATTGTTGAGGCAACGCAAGCTGATCTTTCTCTCTCTCTCC 246
QY 60 CCAATTCGAGGAGCCCGCGGCGTCAATG---GCGCTCTCCGAGCTGGGGTACGC 116
DB 247 CCAATTCGAGGAGCCCGCGGCGTCAATG---GCGCTCTCCGAGCTGGGGTACGC 306
QY 117 GTGAAGCCCGGAGGCTTGCGCGCGGCAAGACCCCAAGGACCACTTTCTGCTTGGAG 176
DB 307 GTGAAGCCCGGAGGCTTGCGCGCGGCAAGACCCCAAGGACCACTTTCTGCTTGGAG 366
QY 177 TTGCTCCCGGCAACCCCGGCGTCTGTCCTTCTCAATCCCAACCGCGGCGGC-CGCGG 235
DB 367 TTGCTCCCGGCAACCCCGGCGTCTGTCCTTCTCAATCCCAACCGCGGCGGC-CGCGG 426
QY 236 ACAAACAAGTTCGCGAGGAGGCTTGCCATTCAGATGCTGAGAGGAGC-GCAGCGGC 294
DB 427 ACAAACAAGTTCGCGAGGAGGCTTGCCATTCAGATGCTGAGAGGAGC-GCAGCGGC 486
QY 295 TCGGTTCTGAGCCCAACCGCA-GCTGAAGGCAATTCGCGTGAATGCTTCGCTAGAGGA 353
DB 487 TCGGTTCTGAGCCCAACCGCAACCGGCTGAAGGCAATTCGCGTGAATGCTTCGCTAGAGGA 546
QY 354 GTGTGAGATGGGATTAACGTCCACATGAGATATGAAGAGAGCCGGGATTTGTAACG 413
DB 547 GTGTGAGATGGGATTAACGTCCACATGAGATATGAAGAGAGCCGGGATTTGTAACG 606
QY 414 TTAACATGTCAGTGGGCTGCTTTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 473
DB 607 TTAACATGTCAGTGGGCTGCTTTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 666
QY 474 CCTGCGCGGCGCTCTCTCACTTCACTTGAAGATACCACTTGAAGGAGGAGGAGGAGGAGG 533
DB 667 CCTGCGCGGCGCTCTCTCACTTCACTTGAAGATACCACTTGAAGGAGGAGGAGGAGGAGG 726
QY 534 CAACCAAAATACCAAAATCTCTCAACCAAGATGTAAGTGTGCTGCTGCTGCTGCTGCTGCT 593
DB 727 CAACCAAAATACCAAAATCTCTCAACCAAGATGTAAGTGTGCTGCTGCTGCTGCTGCTGCT 786
QY 594 AGGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 653
DB 787 AGGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 846
QY 654 TGGGCGCCCAACAATAGAGACAGTCTTATTTGGGAGTACTTGCAGATTAAGGCGCCACAC 713
DB 847 TGGGCGCCCAACAATAGAGACAGTCTTATTTGGGAGTACTTGCAGATTAAGGCGCCACAC 906

QY 714 CTAGAGATCCCGGCTCTATGCTTGTATCTGCCAGTAGACCTGTAGACAGTGAACCTTGGT 773
DB 907 CTAGAGATCCCGGCTCTATGCTTGTATCTGCCAGTAGACCTGTAGACAGTGAACCTTGGT 966
QY 774 ACTTCATGTGATGATGTACAGATGCTCATCTCATCCGAGATGATGAGATGACACCGATG 833
DB 967 ACTTCATGTGATGATGTACAGATGCTCATCTCATCCGAGATGATGAGATGACACCGATG 1026
QY 834 GTGCGGAAGATTTTGTGATGAGAGAACAGTAAACAAAGAGAGGACCACTTCGACCAACA 893
DB 1027 GTGCGGAAGATTTTGTGATGAGAGAACAGTAAACAAAGAGAGGACCACTTCGACCAACA 1086
QY 894 CAGAAAAGATGAAAAGGCGCTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 953
DB 1087 CAGAAAAGATGAAAAGGCGCTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1146
QY 954 GCCCAGCGCGGGGAGCCCAATGCAACCAATGCGGTGGCTGAAAACCGGAGAGATTGA 1013
DB 1147 GCCCAGCGCGGGGAGCCCAATGCAACCAATGCGGTGGCTGAAAACCGGAGAGATTGA 1206
QY 1014 AGCAGAGCATGCTGATGAGGCTTACAGATGACAAACCAAGACCTGAGACCTTATATG 1073
DB 1207 AGCAGAGCATGCTGATGAGGCTTACAGATGACAAACCAAGACCTGAGACCTTATATG 1266
QY 1074 AAGGTGCTCCCATCTGACCAAGGGAATTATACCTGTGTAGTGAATGATATACGGGT 1133
DB 1267 AAGGTGCTCCCATCTGACCAAGGGAATTATACCTGTGTGTGATGATATACGGGT 1326
QY 1134 CCATCAATCACACGTACCACTGATGTTGTGAGAGCAATGCGCTCAACCGGCCATCTCTCC 1193
DB 1327 CCATCAATCACACGTACCACTGATGTTGTGAGAGCAATGCGCTCAACCGGCCATCTCTCC 1386
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QY 1254 AGGTTTACAGTATGAGCCAGCGCCCAACATCAAGTGTATCAACAGTGTATCAACAGGCA 1313
DB 1447 AGGTTTACAGTATGAGCCAGCGCCCAACATCAAGTGTATCAACAGTGTATCAACAGGCA 1506
QY 1314 GTAATTAAGGAGCCGAGCGGCTGCTCACTCAAGGTTCTCAAGCATCTGGGGATTAATA 1373
DB 1507 GTAATTAAGGAGCCGAGCGGCTGCTCACTCAAGGTTCTCAAGGTTCTGAGGCGCGCG 1566
QY 1374 GTTCCATGCA-----GAAGTGTGCTCTGTTCAATGTGACCGAGCGGGA 1419
DB 1567 GTTTCACACACCGCAAAAGATGAGTCTCTATATGGAATGTAACTTTTGAAGGA 1626
QY 1420 TGTGCGGGAATATATATGTAAGTCTCAATTAATATAGGAGGCAACAGTCTGCTG 1479
DB 1627 TGTGCGGGAATATATATGTAAGTCTGCGGGATTTCTATTTGGGATATCTTCACTGCAATG 1686
QY 1480 GCTCATGCTCTGCGCAAAACAGCAGCGCTGGAAGAGAGAGAGAGATTAAGCTTCCCG 1539
DB 1687 GTTGAAGTCTGCG-----AGCGCTGGAAGAGAGAGAGATTAAGCTTCCCG 1737
QY 1540 AGACTAATCTGAGATAGCAATTAATGATATAGAGGCTCTTTTAATGCGCTGATAGTGTGT 1599
DB 1738 AGACTAATCTGAGATAGCAATTAATGATATAGAGGCTCTTTTAATGCGCTGATAGTGTGT 1797
QY 1600 AACAGTCAATCTGATGAG 1659
DB 1788 AACAGTCAATCTGATGAG 1857
QY 1660 GCGTGTGACAAAGTACCAAAAGTATCCCTGCGGAGACG-----GTTTGGCTGGA 1911
DB 1858 GCGTGTGACAAAGTACCAAAAGTATCCCTGCGGAGACG-----GTTTGGCTGGA 1911
QY 1720 GTTCAGCTCTTCATGAATCTCAACACCCGCTGTGTGAGATTAACAACGCTCTCTTC 1779
DB 1912 GTTCAGCTCTTCATGAATCTCAACACCCGCTGTGTGAGATTAACAACGCTCTCTTC 1971
QY 1780 AACGGAGACACCCCAATGCTGAGGAGGCTCCGAGTATGAATTCAGAGAGACCAAA 1839

Db	1972	AAAGGCAAGAC	CCCCATGCTGGACGGGGTCTCCAGATGATCTTCAGAGAACCCAA	2031
Qy	1840	ATGGAGTTTCA	AGAGATAAGCTGACACTGGGCAAGCCCTGGGAGAAAGTTGCTTTGG	1899
Db	2032	ATGGGAGTTTCA	AGAGATTAAGCTGACACTGGGCAAGCCCTGGGAGAAAGTTGCTTTGG	2091
Qy	1900	GCAAGTGTCTAT	GGCGGAGACGTGGGAATTGACAAAGACAAAGCCCAAGAGGGGGCTAC	1959
Db	2092	GCAAGTGTCTAT	GGCGGAGACGTGGGAATTGACAAAGACAAAGCCCAAGAGGGGGCTAC	2151
Qy	1960	CGTGGCCGTGA	AGATGTTGAAGTGAAGTGAAGCCACAGAAACACCTTCTGATCTGGTGC	2019
Db	2152	CGTGGCCGTGA	AGATGTTGAAGTGAAGTGAAGCCACAGAAACACCTTCTGATCTGGTGC	2211
Qy	2020	AGAGATGAGAT	GATGATGAATGATTTGGGAAACACAAAGATATCATTAATCTTCTYGAGC	2079
Db	2212	AGAGATGAGAT	GATGATGAATGATGAATGATTTGGGAAACACAAAGATATCATTAATCTTCTYGAGC	2271
Qy	2080	CTGCACACAG	ATGGGCTTCTATGTCATAGTTGAATGATGCTTAAAGCAACTTCG	2139
Db	2272	CTGCACACAG	ATGGGCTTCTCTATGTCATAGTTGAATGATGCTTAAAGCAACTTCG	2331
Qy	2140	AGATATACCT	CCGAGCGCCGAGGGCCACCCGGGATGAGATCTCTATGACATTAACCGGT	2199
Db	2332	AGATATACCT	CCGAGCGCCGAGGGCCACCCGGGATGAGATCTCTATGACATTAACCGGT	2391
Qy	2200	TCCTGAGAG	AGAGATGACCTTCAAGGACTTGGTGCATGACACTACAGCTGGCCAGAG	2259
Db	2392	TCCTGAGAG	AGAGATGACACTTCAAGGACTTGGTGCATGACACTACAGCTGGCCAGAG	2451
Qy	2260	GATGAGATAC	TCTGGCTTCCAAAAATGATTTATGAGATTTAAGACGCCAGAAATGTTTT	2319
Db	2452	CATGAGATAC	TCTGGCTTCCAAAAATGATTTATGAGATTTAAGACGCCAGAAATGTTTT	2511
Qy	2320	GCTAACAGAAA	CAATGTGATGAAATAGCAGACTTTGGACTGGCAAGATATCAACA	2379
Db	2512	GCTAACAGAAA	CAATGTGATGAAATAGCAGACTTTGGACTGGCAAGATATCAACA	2571
Qy	2380	TATGACATATT	ACAAAAAGACCAACAAATGGGCGCTTCAGTCAAGTGAATGGCTCCAGA	2439
Db	2572	TATGACATATT	ACAAAAAGACCAACAAATGGGCGCTTCAGTCAAGTGAATGGCTCCAGA	2631
Qy	2440	AGCCCTGTTG	ATAGAGTACACTCATCAGAGTATCTGGTCTTCCGGGGTGTTAAT	2499
Db	2632	AGCCCTGTTG	ATAGAGTATAGATATACACTCATCAGAGTATCTGGTCTTCCGGGGTGTTAAT	2691
Qy	2500	GTGGGAGAT	CTTCACTTTAAGGGGGCTGGCCTTACCAGGAAATCCCGTGGAGAACTTT	2559
Db	2692	GTGGGAGAT	CTTCACTTTAAGGGGGCTGGCCTTACCAGGAAATCCCGTGGAGAACTTT	2751
Qy	2560	TAAGTGTGTA	AGGAAGGACACAGAAATGATTAAGCAGACCAACTGACCAACGAACGTGA	2619
Db	2752	TAAGTGTGTA	AGGAAGGACACACAGATGATTAAGCAGACCAACTGACCAACGAACGTGA	2811
Qy	2620	CATGATGATG	AGGGACTGTGGCATGACAGTGGCCCTCCAGAGACCAAGTTCAAGCAATT	2679
Db	2812	CATGATGATG	AGGGACTGTGGCATGACAGTGGCCCTCCAGAGACCAAGTTCAAGCAATT	2871
Qy	2660	GGTAGAGAC	CTTGGATCGAATTTCTCACTCTCAACAACATAGAGAAATCTTGGACCTGAG	2739
Db	2872	GGTAGAGAC	CTTGGATCGAATTTCTCACTCTCAACAACATAGAGAAATCTTGGACCTGAG	2931
Qy	2740	CCAACTCTCG	AAAGATTAACCAAGTTAACCTGACCAAGAAATCTGTTCTTCAAG	2799
Db	2932	CCAACTCTCG	AAAGATTAACCAAGTTAACCTGACCAAGAAATCTGTTCTTCAAG	2991
Qy	2800	AGATGATTTCT	GTGTTTCTCCAGACCCCATGCTTACAGAACCATGCTTCTCAGATATCC	2859
Db	2992	AGATGATTTCT	GTGTTTCTCCAGACCCCATGCTTACAGAACCATGCTTCTCAGATATCC	3051
Qy	2860	ACAATTAAC	CGCAGTGTAAAAATGATGACTGTGTGCTGTCCCAACAGAGCA	2919

Db		3052	ACACATAAAGCGGAGTGTAAATGAATGAATGACTGTCTCCGTCGCCCAAGAGACA	3111
Qy		2920	GCACTGGGAACCTTGACTGCACCTGAGCAGGAGAACAGCCCTCCAGAGCTTGTCGCC	2979
Db		3112	GCACTGGGAACCTTAGCTACACTGAGCAGGAGAACAGCCCTCCAGAGCTTGTCGCC	3171
Qy		2980	ACTGTATATATATGATCAGAGAGTAATATATTGAAAAGTATCACATATGTGTAAG	3039
Db		3172	ACTGTATATATGATCAGAGAGTAATATATTGAAAAGTATCACATATGTGTAAG	3231
Qy		3040	ATTATATACAGTTGAAAACTGTMACTCTCCCAAGAGAGAAGAGGTTTTGAGCAGT	3099
Db		3232	ATTATATACAGTTGAAAACTGTMACTCTCCCAAGAGAGAAGAGGTTTTGAGCAGT	3291
Qy		3100	GGACTGC 3106	
Db		3292	GGACTGC 3298	
			RESULT 8	
			US-10-669-920-628	
			/ Sequence 628, Application US//10669920	
			/ Publication No. US20060194265A1	
			/ GENERAL INFORMATION:	
			/ APPLICANT: Morristo, David W.	
			/ TITLE OF INVENTION: NOVEL THERAPEUTIC TARGETS IN CANCER	
			/ FILE REFERENCE: 20366-066001	
			/ CURRENT APPLICATION NUMBER: US//10/669, 920	
			/ CURRENT FILING DATE: 2003-09-23	
			/ PRIOR APPLICATION NUMBER: US 10/004,113	
			/ PRIOR FILING DATE: 2001-10-23	
			/ PRIOR APPLICATION NUMBER: US 10/052,482	
			/ PRIOR FILING DATE: 2001-11-08	
			/ PRIOR APPLICATION NUMBER: US 09/997,722	
			/ PRIOR FILING DATE: 2001-11-30	
			/ PRIOR APPLICATION NUMBER: US 10/034,650	
			/ PRIOR FILING DATE: 2001-12-20	
			/ PRIOR APPLICATION NUMBER: US 10/085,117	
			/ PRIOR FILING DATE: 2002-02-27	
			/ PRIOR APPLICATION NUMBER: US 10/087,192	
			/ PRIOR FILING DATE: 2002-03-01	
			/ PRIOR APPLICATION NUMBER: US 10/322,281	
			/ PRIOR FILING DATE: 2002-12-17	
			/ PRIOR APPLICATION NUMBER: US 10/322,696	
			/ PRIOR FILING DATE: 2002-12-17	
			/ NUMBER OF SEQ ID NOS: 1441	
			/ SOFTWARE: FastSeq for Windows Version 4.0	
			/ SEQ ID NO 628	
			/ LENGTH: 4998	
			/ TYPE: DNA	
			/ ORGANISM: Homo sapiens	
			US-10-669-920-628	
Qy		1	CCCCGGAGCAAAAGTTGGTGGAGGCAACG-CAGAGCTGAGTCACTTTCTCTCTCGTCCC	59
Db		578	CTCGGAGCAAAAGTTGGTGGAGGCAACGCAAGCTGAGTCACTTTCTCTCTCTCGTCCC	637
Qy		60	CCAATCCGAGGAGGAGCCCGCGGAGCTCATNT--GCGCTCTCCGCAAGCCTGAGGATAGC	116
Db		638	CCAATCCGAGGAGGAGCCCGCGGAGCTCATNTCCCGCGCTCTCCGCAAGCCTGAGGATAGC	697
Qy		117	GTGAAGCCCGGAGGCTTGGCGCGCGGAGGAAGACCAGACACATCTTTCTGCGTTTGAG	176
Db		698	GTGAAGCCCGGAGGCTTGGCGCGCGGAGGAAGACCAGACACATCTTTCTGCGTTTGAG	757
Qy		177	TTCGCTCCCGGAGCCCGGAGGCTGATGCTTTCTGCATCCGAGCAAGCGGAGGCG-CGAGG	235
Db		758	TTCGCTCCCGGAGCCCGGAGGCTGATGCTTTCTGCATCCGAGCAAGCGGAGGCGCGGAG	817

OY 236 ACAACACAGGTGCGGAGAGGCGTTGCCATTCAAGTGACTGACAGCAGC- GCAGCGCC 294
DB 818 ACAACACAGGTGCGGAGAGGCGTTGCCATTCAAGTGACTGACAGCAGCAGCGCGCC 877
OY 295 TCGGTTCTTGAGCCCAACGCA- GCTGAAGGCAATTGCGGTAGTCCATGCCCCGTAGAGAA 353
DB 878 TCGGTTCTTGAGCCCAACGCAAGGCGTAAGGCAATTCGCGGTAGTCCATGCCCCGTAGAGAA 937
OY 354 GGTGSCAATGGGATTAAGTCCACATGAGATATGAAAGAGAACCGGGGATTTGGTACG 413
DB 938 GTGTSCAATGGGATTAAGTCCACATGAGATATGAAAGAGAACCGGGGATTTGGTACG 997
OY 414 TAACCATGATGACGTGGGGTCTGTTTCATCTGCTGGTGTGTGTCACATGGCAACTTGT 473
DB 998 TAACCATGATGACGTGGGGTCTGTTTCATCTGCTGGTGTGTGTCACATGGCAACTTGT 1057
OY 474 CCTGGCCCGGCTCTGCTTCAAGTTAGTTAGAGATACCACTTAAAGCCAGAAAGCCAC 533
DB 1058 CCTGGCCCGGCTCTGCTTCAAGTTAGTTAGAGATACCACTTAAAGCCAGAAAGCCAC 1117
OY 534 CAACCAAAATACCAAAATCTCTCAACAGAAAGTGAAGTGGCTGCGCAGGGAGTGGTAG 593
DB 1118 CAACCAAAATACCAAAATCTCTCAACAGAAAGTGAAGTGGCTGCGCAGGGAGTGGTAG 1177
OY 594 AGGTGCGCTGCTGTTGAAAGATGCGCGCGGTGATCAATTGGACTTAAGATGGGGTGTCACT 653
DB 1178 AGGTGCGCTGCTGTTGAAAGATGCGCGCGGTGATCAATTGGACTTAAGATGGGGTGTCACT 1237
OY 654 TGGGGCCCAACAAATGAGACAGTCTTATTTGGGAGTACTTGCAGATTAAGGGCGCAAC 713
DB 1238 TGGGGCCCAACAAATGAGACAGTCTTATTTGGGAGTACTTGCAGATTAAGGGCGCAAC 1297
OY 714 CTAGAGACTCGGGCTCTATGCTTTGACTGACAGTAGAGCTGTAGACAGTGAACCTTGGT 773
DB 1298 CTAGAGACTCGGGCTCTATGCTTTGACTGACAGTAGAGCTGTAGACAGTGAACCTTGGT 1357
OY 774 ACTTCATGTTGATGTGACAGATGTCATCTCATCCGAGATGATGAGATGACACCGATG 833
DB 1358 ACTTCATGTTGATGTGACAGATGTCATCTCATCCGAGATGATGAGATGACACCGATG 1417
OY 834 GTGCGGAGATTTTGTCAGTGAGAACAGTAACAACAAGAGACCACTTGGACCAACA 893
DB 1418 GTGCGGAGATTTTGTCAGTGAGAACAGTAACAACAAGAGACCACTTGGACCAACA 1477
OY 894 CAGAAAGATGGAAGAAAGCGGCTCAATGCTGTGCTGCGCAACTGTCAAGTTTCGT 953
DB 1478 CAGAAAGATGGAAGAAAGCGGCTCAATGCTGTGCTGCGCAACTGTCAAGTTTCGT 1537
OY 954 GCCCAGCCCGGGGGGAAACCAATGTCACCAATGCGGTGCTGAAAGAAAGGAGTTTA 1013
DB 1538 GCCCAGCCCGGGGGGAAACCAATGTCACCAATGCGGTGCTGAAAGAAAGGAGTTTA 1597
OY 1014 AGCAGAGAGATGCGCATTTGAGAGCTTCAAGTGAAGAAACAGACCTGGACCTCATTAAG 1073
DB 1598 AGCAGAGAGATGCGCATTTGAGAGCTTCAAGTGAAGAAACAGACCTGGACCTCATTAAG 1657
OY 1074 AAAAGTGTGCTCATCTGCAAGAGGAATTAATCACTGTAGTGAAGATGAATACGGGT 1133
DB 1658 AAAAGTGTGCTCATCTGCAAGAGGAATTAATCACTGTGTGTGAGGAATGAATACGGGT 1717
OY 1134 CCATCAATCAACAGTACCACTTGATGTTGTGAGAGGATCGCTCAACCGGCCCATCTTC 1193
DB 1718 CCATCAATCAACAGTACCACTTGATGTTGTGAGAGGATCGCTCAACCGGCCCATCTTC 1777
OY 1194 AAGCCGAGCTGCGGCAATGCTTCAACAGTGTGGAAGAGAGCTTAAGATTGTGTGA 1253
DB 1778 AAGCCGAGCTGCGGCAATGCTTCAACAGTGTGGAAGAGAGCTTAAGATTGTGTGA 1837
OY 1254 AGGTTTACAGTGAATGCGCAGCCACATCCAGTGAATCAAGCAGTGAAGAAAGAGCA 1313
DB 1838 AGGTTTACAGTGAATGCGCAGCCACATCCAGTGAATCAAGCAGTGAAGAAAGAGCA 1897

OY 1314 GTAAATACGGGCCCCAGGGGCTGCTTACCTCAAGTTCTCAAGCACTCGGGGATTAATA 1373
DB 1898 GTAAATACGGGCCCCAGGGGCTGCTTACCTCAAGTTCTCAAGTTCTTAAAGGCGCCG 1957
OY 1374 GTTCCAATGCA-----GAAAGTCTGGCTCTGTTCATGTTGAACCGAGCGGA 1419
DB 1958 TGTTTACACACGGAACAAAGAGATGAGGTTCTCTATATTGCGAATGTTAACTTTGAGGA 2017
OY 1420 TGTGGGAAATATATATGTTAAAGTCTTCCATTATATATGCGGACGACCAACAGTGTCTG 1479
DB 2018 CGCTGGGAAATATACGTGTCTGGCTGGGTAATCTTATTTGGAGATATCTTTCACTGTGATG 2077
OY 1480 GCTACGTCTCTGCAAAACAGAGCGCTGGAAGAGAAAGAGATTACAGCTTCCC 1539
DB 2078 GTTACAGTTCTGCC-----AGCGCTGGAAGAGAAAGAGATTACAGCTTCCC 2128
OY 1540 AGACTACCTGGAGATGACCATTTTACTGATAGGGGTCTTCTTAATGCGCTGTATGTGT 1599
DB 2129 AGACTACCTGGAGATGACCATTTTACTGATAGGGGTCTTCTTAATGCGCTGTATGTGT 2188
OY 1600 AACAGTATCTGTGCGGAATGAAGAACAGACCAAGAGCCAGACTTTCAGACCCAGCC 1659
DB 2189 AACAGTATCTGTGCGGAATGAAGAACAGACCAAGAGCCAGACTTTCAGACCCAGCC 2248
OY 1660 GGTGTGACAGAGCTGACCAACGATCCCTGCGGAGACAGGTAAAGTTTGCGCTGA 1719
DB 2249 GGTGTGACAGAGCTGACCAACGATCCCTGCGGAGACAGGTAAAGTTTGCGCTGA 2302
OY 1720 GTCCAGCTCTCATGAACTTCAACACCCCGCTGGTGAAGATTAACAACGCGCTCTTTC 1779
DB 2303 GTCCAGCTCTCATGAACTTCAACACCCCGCTGGTGAAGATTAACAACGCGCTCTTTC 2362
OY 1780 AACGCGACACACCCCATGCTGCGAGGGGTCTCCGAGTATTAATTCCAGAGAACCAAA 1839
DB 2363 AACGCGACACACCCCATGCTGCGAGGGGTCTCCGAGTATTAATTCCAGAGAACCAAA 2422
OY 1840 ATGGAGTTTCCAAAGATTAAGCTGACACTGGGCAAGCCCTGGGAGAGAGGTTCTTTGG 1899
DB 2423 ATGGAGTTTCCAAAGATTAAGCTGACACTGGGCAAGCCCTGGGAGAGAGGTTCTTTGG 2482
OY 1900 GCAAGTGTCAATGCGGAGAGAGTGGGAATTTGAACAAGACCAAGCCCAAGAGCGGTAC 1959
DB 2483 GCAAGTGTCAATGCGGAGAGAGTGGGAATTTGAACAAGACCAAGCCCAAGAGCGGTAC 2542
OY 1960 CGTGCCCGTGAAGATGTTGAAGATGATGACACAGAAACAACCTTTCTGTATGTCGTGTC 2019
DB 2543 CGTGCCCGTGAAGATGTTGAAGATGATGACACAGAAACAACCTTTCTGTATGTCGTGTC 2602
OY 2020 AGAGATGAGAGATGATGAAGATGATTGGGAAACAACAAGATATCAATTAATCTTTGGAGC 2079
DB 2603 AGAGATGAGAGATGATGAAGATGATTGGGAAACAACAAGATATCAATTAATCTTTGGAGC 2662
OY 2080 CTGCAACAGAGATGGGCTCTCTATGTATAGTTAGTATGCTCTTAAGGCAACTTCG 2139
DB 2663 CTGCAACAGAGATGGGCTCTCTATGTATAGTTAGTATGCTCTTAAGGCAACTTCG 2722
OY 2140 AGAATATCTCCGAGCCCGGAGGCAACCCGAGATGAGATCTTCTATGACATTAACCGGT 2199
DB 2723 AGAATATCTCCGAGCCCGGAGGCAACCCGAGATGAGATCTTCTATGACATTAACCGGT 2782
OY 2200 TCTCGAGAGAGAGATGACCTTCAAGGACTTGGGTGATGACCTTCAAGCTGGCCAGAGC 2259
DB 2783 TCTCGAGAGAGAGATGACCTTCAAGGACTTGGGTGATGACCTTCAAGCTGGCCAGAGC 2842
OY 2260 GATGAGTACTTGTGCTTCCAAAAATGTAATTCATGAGATTTAGCAGCCAGAAATGTTT 2319
DB 2843 CATGAGATACTTGTGCTTCCAAAAATGTAATTCATGAGATTTAGCAGCCAGAAATGTTT 2902
OY 2320 GGTAAACAGAAACAAATGATGAAGAAATAGCAGACTTTGATCTGCGCAGAGATTAACA 2379
DB 2903 GGTAAACAGAAACAAATGATGAAGAAATAGCAGACTTTGATCTGCGCAGAGATTAACA 2962
OY 2380 TATAGACTATTAACAAAAGAACCAACATGGGGGCTTCAAGTCAAGTGGATGCTCAGA 2439

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Db      2963 TATGACTATTTAAAGAGACCAACCAATGAGGCGGCTTCAGTCAAGTATGCTCCAGA 3022
Qy      2440 AGCCCTGTTTATAGATATACATCATAGATGATGTCTGCTTCGCGGGTGTAAAT 2499
Db      3023 AGCCCTGTTTATAGATATACATCATAGATGATGTCTGCTTCGCGGGTGTAAAT 3082
Qy      2500 GTGGAGATCTTCACTTTAGGGGGCTGCGCTTACCCAGGATTCCTCGTGAAGAACTTTT 2559
Db      3083 GTGGAGATCTTCACTTTAGGGGGCTGCGCTTACCCAGGATTCCTCGTGAAGAACTTTT 3142
Qy      2560 TAACTGCTGAGAGAGACACAGATGATTAAGCCAGCCAACTGACCAACCACTGTA 2619
Db      3143 TAACTGCTGAGAGAGACACAGATGATTAAGCCAGCCAACTGACCAACCACTGTA 3202
Qy      2620 CATGATGATGAGGAGCTGTTGGCAGTGCAGTCCCTCCAGAGACCAAGCTTCAAGCAGT 2679
Db      3203 CATGATGATGAGGAGCTGTTGGCAGTGCAGTCCCTCCAGAGACCAAGCTTCAAGCAGT 3262
Qy      2680 GGTAGAGACTTGTGATGAAATTTCTCACTTCAACCAATGAGAGAAATCTTGGACCTCAG 2739
Db      3263 GGTAGAGACTTGTGATGAAATTTCTCACTTCAACCAATGAGAGAAATCTTGGACCTCAG 3322
Qy      2740 CCAACCTCTGAGACAGATTCACCTAGTTACCTGACACAAAGATTTCTTCTCAGG 2799
Db      3323 CCAACCTCTGAGACAGATTCACCTAGTTACCTGACACAAAGATTTCTTCTCAGG 3382
Qy      2800 AGATGATTCGTTTCTTCAGACCCCATGCTTACCAACCAATGCTTCTCAGATTC 2859
Db      3383 AGATGATTCGTTTCTTCAGACCCCATGCTTACCAACCAATGCTTCTCAGATTC 3442
Qy      2860 ACAATTAACGCGAGTGTAAACATGATGATGCTGTCTGCTGTCCCAACAGAGACA 2919
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Qy      2920 GCACTGGAGAACTAGTACACCTGAGCAGGAGACCAATGCTCCCAAGAGCTTGTGTCTC 2979
Db      3503 GCACTGGAGAACTAGTACACCTGAGCAGGAGACCAATGCTCCCAAGAGCTTGTGTCTC 3562
Qy      2980 ACTTGTATATATGATCAGAGAGTAAATATTTGAAAGATATCAGCATATGTGTAAAG 3039
Db      3563 ACTTGTATATATGATCAGAGAGTAAATATTTGAAAGATATCAGCATATGTGTAAAG 3522
Qy      3040 ATTATTAAGTTGAAAATCTGTATCTTCCCAAGAGAGAAAGGTTTCTGAGAGACT 3099
Db      3623 ATTATTAAGTTGAAAATCTGTATCTTCCCAAGAGAGAAAGGTTTCTGAGAGACT 3682
Qy      3100 GGAAGTC 3106
Db      3683 GGAAGTC 3689

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RESULT 9
US-10-669-920-590

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; Sequence 590, Application US/10669920
; Publication No. US20060194265A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
; APPLICANT: Malandro, Marc S.
; TITLE OF INVENTION: NOVEL THERAPEUTIC TARGETS IN CANCER
; FILE REFERENCE: 20366-066001
; CURRENT APPLICATION NUMBER: US/10/669,920
; PRIORITY FILING DATE: 2003-09-23
; PRIOR APPLICATION NUMBER: US 10/004,113
; PRIOR FILING DATE: 2001-10-23
; PRIOR APPLICATION NUMBER: US 10/052,482
; PRIOR FILING DATE: 2001-11-08
; PRIOR APPLICATION NUMBER: US 09/997,722
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: US 10/034,650
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: US 10/085,117
; PRIOR FILING DATE: 2002-02-27

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; PRIOR APPLICATION NUMBER: US 10/087,192
; PRIOR FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 10/322,281
; PRIOR FILING DATE: 2002-12-17
; PRIOR APPLICATION NUMBER: US 10/322,696
; PRIOR FILING DATE: 2002-12-17
; NUMBER OF SEQ ID NOS: 1441
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 590
; LENGTH: 4472
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-669-920-590

Query Match      90.9%; Score 2824.2; DB 6; Length 4472;
Best Local Similarity 97.0%; Pred. No. 0;
Matches 2970; Conservative 0; Mismatches 63; Indels 28; Gaps 8;

Qy      1 CCGGAGGCAAGTTGTTGAGAGCAAG-CAAGCTGATCTTCTCTCTCTCC 59
Db      578 CTGGGAGCAAGTTGTTGAGAGCAAGCTGATCTTCTCTCTCTCTCC 637
Qy      60 CCAATCCGAGGAGCAGCCCGCGGCGTCAAG--GCGCTCTCCGAGCTGCGGTAAGC 116
Db      638 CCAATCCGAGGAGCAGCCCGCGGCGTCAAGCCCGGCTCTCCGAGCTGCGGTAAGC 697
Qy      117 GTGAAGCCCGGAGGCTTGGCGCCGCGCAAGACCAAGAGACCACTTCTGCGTTGAG 176
Db      698 GTGAAGCCCGGAGGCTTGGCGCCGCGCAAGACCAAGAGACCACTTCTGCGTTGAG 757
Qy      177 TTGCTCCCGCAACCCCGGGCTGTGCTTCTCCATCCGACCCAGCGGGGAC-CGGG 235
Db      758 TTGCTCCCAACCCCGGGCTGTGCTTCTCCATCCGACCCAGCGGGGACCGGG 817
Qy      236 ACAACAGAGTCCGAGAGAGCGTTCATCAAGTCACTGACAGCAGC-GCAGCGCT 294
Db      818 ACAACAGAGTCCGAGAGAGCGTTCATCAAGTCACTGACAGCAGCAGCGCGC 877
Qy      295 TGGTCTCTGAGCCCAACCGCA-CTGAAGGCAATGGCGCTTCTCCATGGCGGAGAA 353
Db      878 TGGTCTCTGAGCCCAACCGCACTGAAGGCAATGGCGCTTCTCCATGGCGGAGAA 937
Qy      354 GTGTGAGATGAGATTAAGTCAATGAGATGAGAGAGACCGGGATTTGTACCG 413
Db      938 GTGTGAGATGAGATTAAGTCAATGAGATGAGAGAGACCGGGATTTGTACCG 997
Qy      414 TAACCATGTCAGCTGGGGTGTCTCATCTGCTGTGTCATGATGAGCAACTGT 473
Db      998 TAACCATGTCAGCTGGGGTGTCTCATCTGCTGTGTCATGATGAGCAACTGT 1057
Qy      474 CCTGGCCCGGCTCTCTCAAGTTTATGAGATACCAATTAAGCCAGAGAGCCAC 533
Db      1058 CCTGGCCCGGCTCTCTCAAGTTTATGAGATACCAATTAAGCCAGAGAGCCAC 1117
Qy      534 CAACCAATTAACCAATCTCTCAACCAAGATGATGAGTGGCGCAGGGAGTGTCTAG 593
Db      1118 CAACCAATTAACCAATCTCTCAACCAAGATGATGAGTGGCGCAGGGAGTGTCTAG 1177
Qy      594 AGGTGCGTCTGCTGTGAAGATGCGCGGTATCATGTTGATGATGAGATGGGTGACT 653
Db      1178 AGGTGCGTCTGCTGTGAAGATGCGCGGTATCATGTTGATGATGAGATGGGTGACT 1237
Qy      654 TGGGGCCCAACCAATGAGCAGTGTCTTATTTGGGAGTATCTTGCAGATTAAGGGCGCAC 713
Db      1238 TGGGGCCCAACCAATGAGCAGTGTCTTATTTGGGAGTATCTTGCAGATTAAGGGCGCAC 1297
Qy      714 CTAGAGACTCCGGGCTCTAGCTTGTACTGACAGTGAAGCTGTAAGCACTGTGT 773
Db      1298 CTAGAGACTCCGGGCTCTAGCTTGTACTGACAGTGAAGCTGTAAGCACTGTGT 1357
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Qy 834 GTGCGAAGATTTTGTCAGTGAGAA CAGTAA CAAAGAGACACATACCTGAGCAACA 893
Db 1418 GTGCGGAAGATTTTGTCAGTGAGAA CAGTAA CAAAGAGAGACACATACCTGAGCAACA 1477
Qy 894 CAGAAAGATGGAAGAGGGCTCCATGCTGTGCTGCGGGCCAA CACTGTCAAGTTTCCT 953
Db 1478 CAGAAAGATGGAAGAGGGCTCCATGCTGTGCTGCGGGCCAA CACTGTCAAGTTTCCT 1537
Qy 954 GCCACCGCGGGGGGAAACCAATGCCAATCGGTGCTGAAAAACGGGAGAGATTTA 1013
Db 1538 GCCACCGCGGGGGGAAACCAATGCCAATCGGTGCTGAAAAACGGGAGAGATTTA 1597
Qy 1014 AGCAGAGCATGCAATTGAGGCTCA CAAAGTACGAAACCAAGCATGAGACCTCATTTATG 1073
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Qy 1074 AAAGTGTGTCCTCATCTGCAAGGGAAATTAACCTGTGTAGTTGAGAAATGAATACGGGT 1133
Db 1658 AAAGTGTGTCCTCATCTGCAAGGGAAATTAACCTGTGTGTGAGAAATGAATACGGGT 1717
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Db 1778 AAGCGGACCTGCGGCAATGCTCTCA CAGTGTGAGAGAGACGTAAGATTGTCTGCA 1837
Qy 1254 AGGTTTACAGTATGCCAGGCCCAATCAGTGTGATCAAGACCGTGGAAAAAGAACGGCA 1313
Db 1838 AGGTTTACAGTATGCCAGGCCCAATCAGTGTGATCAAGACCGTGGAAAAAGAACGGCA 1897
Qy 1314 GTAAATACCGGGCCCGACGGGCTGACCTCAAGGTTCTCAAGACCTCGGGGATTAATA 1373
Db 1898 GTAAATACCGGGCCCGACGGGCTGACCTCAAGGTTCTCAAGGCTCGGGGATTAATA 1957
Qy 1374 GTTCCATGCAAGAGTGTGCTGTGT-----TCAATGTACCGAGCGGATGCTGGG 1427
Db 1958 CCACGGACCAAGAGATTGAGGTTCTATATTCGGAATGTAACTTTTGGAGACGCTGGGG 2017
Qy 1428 AATATATATGTAAGTCTCAATTAATATAGGCAAGGCCAA CAGTGTGCTGATCAGTCA 1487
Db 2018 AATATATGCTTGGCGGGTAAATCTATGTGGAATATCTTTCACTCTGATGATTGAAG 2077
Qy 1488 TCTTCGCAAAACAGCAGAGCGCTGAGAGAGAAAGAGATTACAGTTTCCCAAGTACC 1547
Db 2078 TTTCTGCT-----AGCGCTGGAGAGAGAAAGAGATTACAGTTTCCCAAGTACC 2128
Qy 1548 TGGAGATGACATTTATCTGATAGGGGTCTTTTAATGCGCTGTATGTGTATACGTCA 1607
Db 2128 TGGAGATGACATTTATCTGATAGGGGTCTTTTAATGCGCTGTATGTGTATACGTCA 2188
Qy 1608 TCTGTGCGGATGTAAGAACAGACCAAGACGAGACTTCAGCGCCAGCGGGCTGTGC 1667
Db 2188 TCTGTGCGGATGTAAGAACAGACCAAGACGAGACTTCAGCGCCAGCGGGCTGTGC 2248
Qy 1668 ACAAGGTGACAAACGTTATCCCTCTGCGAGACAGGTAA CAGTTTCGCTGATCCAGCT 1727
Db 2249 ACAAGGTGACAAACGTTATCCCTCTGCGAGACAG-----GTTTCGCTGATCCAGCT 2302
Qy 1728 CCTTCATGAATCTCAACACCCCGCTGTGTAGATTAACA CAGGCTCTCTTCAACGGCAG 1787
Db 2303 CCTTCATGAATCTCAACACCCCGCTGTGTAGATTAACA CAGGCTCTCTTCAACGGCAG 2362
Qy 1788 ACAACCCCATGCTGCGAGGGGTCTCGAGATGAATTCACAGAGACCAAAATGGAGAT 1847
Db 2363 ACAACCCCATGCTGCGAGGGGTCTCGAGATGAATTCACAGAGACCAAAATGGAGAT 2422
Qy 1848 TTCCAGAGATTAAGCTGACACTGTGGCAAGCCCTGTGGAGAGAGGTTGCTTTGGGCAATGTG 1907
Db 2423 TTCCAGAGATTAAGCTGACACTGTGGCAAGCCCTGTGGAGAGAGGTTGCTTTGGGCAATGTG 2482

Qy 1908 TCATGCGGAAGCAGTGGGAATTGACAAAGACAGGCCAAGGAGCGGTGACCGTGGCGG 1967
Db 2483 TCATGCGGAAGCAGTGGGAATTGACAAAGACAGGCCAAGGAGCGGTGACCGTGGCGG 2542
Qy 1968 TGAAGATGTTGAAGATGATGCTCCAGAGAAAGACCTTTCTGATCTGTGTCAAGATGG 2027
Db 2543 TGAAGATGTTGAAGATGATGCTCCAGAGAAAGACCTTTCTGATCTGTGTCAAGATGG 2602
Qy 2028 AGATGATGAAGATGATTTGGGAAACAAGAAATATCATTAATCTTTCTTGGAGCTGCACAC 2087
Db 2603 AGATGATGAAGATGATTTGGGAAACAAGAAATATCATTAATCTTTCTTGGAGCTGCACAC 2662
Qy 2088 AGAATGGGCTCTCATGTGCTAAGTGTGCTCTAAAGGCAACTCCGAGAAATACC 2147
Db 2663 AGAATGGGCTCTCATGTGCTAAGTGTGCTCTAAAGGCAACTCCGAGAAATACC 2722
Qy 2148 TCCAGACCCGAGGACCAACCCGGAGTGAAGTACTCTTAATGACATTAACGTTGTTCTGAGG 2207
Db 2723 TCCAGACCCGAGGACCAACCCGGAGTGAAGTACTCTTAATGACATTAACGTTGTTCTGAGG 2782
Qy 2208 AGCAGATGACCTTCAAGGACTTGTGTATGCACTTACAGCTGTGCGCAGACGATGGAGT 2267
Db 2783 AGCAGATGACCTTCAAGGACTTGTGTATGCACTTACAGCTGTGCGCAGACGATGGAGT 2842
Qy 2268 ACTTGGGCTTCCCAAAATGTAATTCATGAGATTAGACGACGAGAAATGTTTGGTAAACAG 2327
Db 2843 ACTTGGGCTTCCCAAAATGTAATTCATGAGATTAGACGACGAGAAATGTTTGGTAAACAG 2902
Qy 2328 AAAACAATGTATGATAAATAGACAGACTTTGGAATCTGCGCAGAGATTAACAATATTAAGT 2387
Db 2903 AAAACAATGTATGATAAATAGACAGACTTTGGAATCTGCGCAGAGATTAACAATATTAAGT 2962
Qy 2388 ATTACAAAAAACAACCAATGTGGGCTTCCAGTCAAGTGAATGGCTTCCAGAAACCCCTGT 2447
Db 2963 ATTACAAAAAACAACCAATGTGGGCTTCCAGTCAAGTGAATGGCTTCCAGAAACCCCTGT 3022
Qy 2448 TTGATGATGATTAACATCATCAGATGATGATGCTGATGCTGCTGGGGGTGTTAATGTGGAGA 2507
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Qy 2508 TCTTCACTTTAGGGGGCTGCGCTTACCCAGGGAATTCGCGTGGAGAACTTTTAAAGCTGC 2567
Db 3083 TCTTCACTTTAGGGGGCTGCGCTTACCCAGGGAATTCGCGTGGAGAACTTTTAAAGCTGC 3142
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Qy 2688 ACTTGGATCGAATTTCTCACTCTCAACCAATGAGAAATACCTTGAACCTTCAGCCAACTTC 2747
Db 3263 ACTTGGATCGAATTTCTCACTCTCAACCAATGAGAAATACCTTGAACCTTCAGCCAACTTC 3322
Qy 2748 TCGAAACGATTAATCACTTAATCTGACCAAGAAATCTTTGTTCTTACAGAGATGATT 2807
Db 3323 TCGAAACGATTAATCACTTAATCTGACCAAGAAATCTTTGTTCTTACAGAGATGATT 3382
Qy 2808 CTGTTTTTCTCGAGACCCAGTGCCTTACGAACCATGCTCTCATGATCCACATTA 2867
Db 3383 CTGTTTTTCTCGAGACCCAGTGCCTTACGAACCATGCTCTCATGATCCACATTA 3442
Qy 2868 ACGCAGTGTAAACATGAATGAATGTGTGCTGCTGCTGCCAAACAGACAGACACTGGG 2927
Db 3443 ACGCAGTGTAAACATGAATGAATGTGTGCTGCTGCTGCCAAACAGACAGACACTGGG 3502
Qy 2928 AACCTAGCTAACAAGAGAGGAGACATGCTCTCCAGAGCTTGTGTCTTCACTTGAT 2987
Db 3503 AACCTAGCTAACAAGAGAGGAGACATGCTCTCCAGAGCTTGTGTCTTCACTTGAT 3562
Qy 2988 AATGAGATCAAGAGATTAATTAATTGAAAGTATACGATATGTGTAAGATTATATAC 3047

DB 3563 AATGATGAGAGAGTAAATATGGAAGAAATGACATATGTATTAATATAC 3622
QY 3048 A 3048
DB 3623 A 3623

RESULT 10
US-10-669-920-598
Sequence 598, Application US/10669920
Publication No. US20060194265A1
GENERAL INFORMATION:
APPLICANT: Moritz, David W.
APPLICANT: Malandro, Marc S.
TITLE OF INVENTION: NOVEL THERAPEUTIC TARGETS IN CANCER
FILE REFERENCE: 20366-066001
CURRENT APPLICATION NUMBER: US/10/669,920
CURRENT FILING DATE: 2003-09-23
PRIOR APPLICATION NUMBER: US 10/004,113
PRIOR FILING DATE: 2001-10-23
PRIOR APPLICATION NUMBER: US 10/052,482
PRIOR FILING DATE: 2001-11-08
PRIOR APPLICATION NUMBER: US 09/997,722
PRIOR FILING DATE: 2001-11-30
PRIOR APPLICATION NUMBER: US 10/034,650
PRIOR FILING DATE: 2001-12-20
PRIOR APPLICATION NUMBER: US 10/085,117
PRIOR FILING DATE: 2002-02-27
PRIOR APPLICATION NUMBER: US 10/087,192
PRIOR FILING DATE: 2002-03-01
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PRIOR FILING DATE: 2002-12-17
PRIOR APPLICATION NUMBER: US 10/322,696
PRIOR FILING DATE: 2002-12-17
NUMBER OF SEQ ID NOS: 1441
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 598
LENGTH: 5080
TYPE: DNA
ORGANISM: Homo sapiens
US-10-669-920-598

Query Match 89.5%; Score 2780.2; DB 6; Length 5080;
Best Local Similarity 94.3%; Pred. No. 0;
Matches 3028; Conservative 0; Mismatches 63; Indels 120; Gaps 9;

QY 1 CCGGAGAGAAATTTGGTGGAGGCAACG-CAGGCTGAGTCTTCTTCTCGTTC 59
DB 578 CTGCGAGCAAAATTTGGTGGAGGCAACGCGAAGCTGAGTCTTCTTCTCTCGTTC 637
QY 60 CCAAAATCCGAGGCGACCGCGCGGCGTCAATG--GGGCTCTCCGAGCGCTGGAGTACG 116
DB 638 CCAAAATCCGAGGCGACCGCGCGGCGTCAATGCGCGGCTCTCCGAGCGCTGGAGTACG 697
QY 117 GTGAACCCCGGAGGCTTGGCGCGCGGAGAACCCCAAGACCACTTTTGTGCGTTTGGAG 176
DB 698 GTGAACCCCGGAGGCTTGGCGCGCGGAGAACCCCAAGACCACTTTTGTGCGTTTGGAG 757
QY 177 TTGCTCCCGCAACCCCGGCGCTGTGCTTTCATCCCGAACCGCGGCGGCG 235
DB 758 TTGCTCCCGCAACCCCGGCGCTGTGCTTTCATCCCGAACCGCGGCGGCGGCG 817
QY 236 ACAACACAGGTCCGCGAGGAGCGTTGCATTCAAGTACGTGACGACGACG-C-GCAGCGCC 294
DB 818 ACAACACAGGTCCGCGAGGAGCGTTGCATTCAAGTACGTGACGACGACGCGCAGCGCC 877
QY 295 TCGGTTCTGAGCCCGACCGCA-GCTGAAGGCAATTTGGCGGTGATCCATGCCGTTAGAGAA 353
DB 878 TCGGTTCTGAGCCCGACCGCGAGGCTGAAGGCAATTTGGCGGTGATCCATGCCGTTAGAGAA 937
QY 354 GTGTGAGATGGATTAAGCTTCAATGAGATATGAGAGAGACCGGGGATGTGATCCG 413

DB 938 GTGTGAGATGGATTAAGCTTCAATGAGATATGAGAGAGACCGGGGATGTGATCCG 997
QY 1414 TAAACATGTCAGCTGGGATGCTTTCATCTGCTGGTGTGATGACATGCAACCTTGT 473
DB 998 TAAACATGTCAGCTGGGATGCTTTCATCTGCTGGTGTGATGACATGCAACCTTGT 1057
QY 474 CCTGGCCCGGCGCTCTTCAAGTTAGTGAAGATACCAATTAGAGCCAGAGGACCA 533
DB 1058 CCTGGCCCGGCGCTCTTCAAGTTAGTGAAGATACCAATTAGAGCCAGAGGACCA 1117
QY 534 CAACCAATATACCAATCTCTCAACCAAGATGATGCTGCGCAGAGGATGCTGAG 593
DB 1118 CAACCAATATACCAATCTCTCAACCAAGATGATGCTGCGCAGAGGATGCTGAG 1177
QY 594 AGTGGCGTGCCTGTGTAAGATGCGCGGATGATGATGATGATGATGATGATGATGATGAT 653
DB 1178 AGTGGCGTGCCTGTGTAAGATGCGCGGATGATGATGATGATGATGATGATGATGATGAT 1237
QY 654 TGGGCGCCCAATAGACAGTGTCTTATTTGGGAGTACTTGCAGATTAAGGGCGCACAC 713
DB 1238 TGGGCGCCCAATAGACAGTGTCTTATTTGGGAGTACTTGCAGATTAAGGGCGCACAC 1297
QY 714 CTAGAGACTCGGCGCTTATGCTTGTACTGCGAGTGAACCTGTGACAGTGAACCTTGT 773
DB 1298 CTAGAGACTCGGCGCTTATGCTTGTACTGCGAGTGAACCTGTGACAGTGAACCTTGT 1357
QY 774 ACTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 833
DB 1358 ACTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1417
QY 834 GTGCGAAGATTTTGTCAGTGAGAACAGTAAACAAGAGAGACACATATCTGACCAACA 893
DB 1418 GTGCGAAGATTTTGTCAGTGAGAACAGTAAACAAGAGAGACACATATCTGACCAACA 1477
QY 894 CAGAAAGATGAGAAAGCGGCTCCATGCTGTGCTGCGGCAACCTGTCAAGTTTCGT 953
DB 1478 CAGAAAGATGAGAAAGCGGCTCCATGCTGTGCTGCGGCAACCTGTCAAGTTTCGT 1537
QY 954 GCCGACCGCGGGGAGAACCAATGCCAATGCGGCTGTAAGAAAGGAGAGTTTA 1013
DB 1538 GCCGACCGCGGGGAGAACCAATGCCAATGCGGCTGTAAGAAAGGAGAGTTTA 1597
QY 1014 AGCAGAGCATGCTGATGAGGCTCAAGGTACGAACACAGACCTGAGCTCATATTAG 1073
DB 1598 AGCAGAGCATGCTGATGAGGCTCAAGGTACGAACACAGACCTGAGCTCATATTAG 1657
QY 1074 AAGTGTGTCCCATCTGACCAAGGAAATTAATCTGTGTATGAGAAATTAACGGGT 1133
DB 1658 AAGTGTGTCCCATCTGACCAAGGAAATTAATCTGTGTATGAGAAATTAACGGGT 1717
QY 1134 CATCAATACACGTAACCTGATGATGTTGTGAGACCATGCGTCAACCGCCCATCTTC 1193
DB 1718 CATCAATACACGTAACCTGATGATGTTGTGAGACCATGCGTCAACCGCCCATCTTC 1777
QY 1194 AAGCGGACTGCGGCAATGCTCTCAAGTGTGAGAGACCTGAGATTGTCTGCA 1253
DB 1778 AAGCGGACTGCGGCAATGCTCTCAAGTGTGAGAGACCTGAGATTGTCTGCA 1837
QY 1254 AGGTTTACAGTATGCCAGCCCAATCCTCACTGATGATCAAGACGTTGAAAGAACGCGCA 1313
DB 1838 AGGTTTACAGTATGCCAGCCCAATCCTCACTGATGATCAAGACGTTGAAAGAACGCGCA 1897
QY 1314 GTTAATTAAGGCGGCGAGCGGCTGCTCAAGTGTCTCAAGACGTTGAAAGAACGCGCA 1373
DB 1898 GTTAATTAAGGCGGCGAGCGGCTGCTCAAGTGTCTCAAGGCGGCGGTTTAAACA 1957
QY 1374 GTTCAATGCAAGATGCTGCTGT-----TCAATGTGACCGAGCGGATGCTGCGG 1427
DB 1958 CCAAGGCAAAAGATGAGGTTCTTAATTCGAAATGTAATCTTTAGAGAGCGCTGGGG 2017
QY 1428 AATATATATATGTAAGTCTTCAATTAATTAAGGAGCGCAACAGTGTGCTGCTCACTG 1487
DB 2018 AATATATGCTTGTGGCGGGTAAATTCATTTGGGATATCTTTCACTGTGATGATGACAG 2077

QY 1488 TCCTGCCAAGACAGACGCGCTGGAGAGAAAGAGATTACAGCTTCCCCAGACTAC 1547
 DB 2078 TTCTGCC-----AGCGCTGGAGAGAAAGAGATTACAGCTTCCCCAGACTAC 2128
 QY 1548 TGGAGATAGCCATTACTGTCATAGGGGCTTTCTTAATGCCCTGTATAGGTGTAAACAGCA 1607
 DB 2129 TGGAGATAGCCATTACTGTCATAGGGGCTTTCTTAATGCCCTGTATAGGTGTAAACAGCA 2188
 QY 1608 TCCTGTGCCAATGAAAGACAGACCAAGAACAGCTTACAGACAGCCAGCGCTGTGC 1667
 DB 2189 TCCTGTGCCAATGAAAGACAGACCAAGAACAGCTTACAGACAGCCAGCGCTGTGC 2248
 QY 1668 ACAACCTGACCAACGATATCCCTCTGCGAGACAGGTAAAGTTTCGCTGAGTCAAGCT 1727
 DB 2249 ACAACCTGACCAACGATATCCCTCTGCGAGACAG-----GTTTCGCTGAGTCAAGCT 2302
 QY 1728 CCTGCATGAACTCCAAACACCCCGCTGTGTAGAGATTAACAACAGCTCTCTTCAACGGCAG 1787
 DB 2303 CCTGCATGAACTCCAAACACCCCGCTGTGTAGAGATTAACAACAGCTCTCTTCAACGGCAG 2362
 QY 1788 ACAACCCCAATGCTGAGGGGGCTCCGAGATGAACCTTCAGAGAGACCAAAATGAGAGT 1847
 DB 2363 ACAACCCCAATGCTGAGGGGGCTCCGAGATGAACCTTCAGAGAGACCAAAATGAGAGT 2422
 QY 1848 TTCCAAGAGATTAAGCTGACACTGCGCAGACCCCTGGAGAGAGTTCTTTGGGCAAGTGG 1907
 DB 2423 TTCCAAGAGATTAAGCTGACACTGCGCAGACCCCTGGAGAGAGTTCTTTGGGCAAGTGG 2482
 QY 1908 TCATGCGGAGAGAGAGTGGGAATTGACAAAGACAGCCCAAGAGGCGTCAACCTGTGCGG 1967
 DB 2483 TCATGCGGAGAGAGAGTGGGAATTGACAAAGACAGCCCAAGAGGCGTCAACCTGTGCGG 2542
 QY 1968 TGAAGAGTGTAAAGATGATGACAGAGAAAGACCTTCTGATCTGCTGAGAGATGG 2027
 DB 2543 TGAAGAGTGTAAAGATGATGACAGAGAAAGACCTTCTGATCTGCTGAGAGATGG 2602
 QY 2028 AGATGATGAAGATGATTTGGGAAACACAGAAATATCAATAATCTTTGGAGCCTGACAC 2087
 DB 2603 AGATGATGAAGATGATTTGGGAAACACAGAAATATCAATAATCTTTGGAGCCTGACAC 2662
 QY 2088 AGATGAGGCTCTCTATGTCTATAGTGTAGTATGCTTAAAGGCACTCCGAGATAC 2147
 DB 2663 AGATGAGGCTCTCTATGTCTATAGTGTAGTATGCTTAAAGGCACTCCGAGATAC 2722
 QY 2148 TCCGAGCCCGAGAGCCAGCCGGATGAGATCTCTATGACATTAACGCTGTCTGAGG 2207
 DB 2723 TCCGAGCCCGAGAGCCAGCCGGATGAGATCTCTATGACATTAACGCTGTCTGAGG 2782
 QY 2208 AGCAGATGACCTTCAAGAGACTTGTGTCTATGACACTTACAGCTGCGCAGACGGATGAGT 2267
 DB 2783 AGCAGATGACCTTCAAGAGACTTGTGTCTATGACACTTACAGCTGCGCAGACGGATGAGT 2842
 QY 2268 ACTTGCTTCCCAAAATGATTCATGAGATTTAGACGCGAGAAATGTTTTGTAAAG 2327
 DB 2843 ACTTGCTTCCCAAAATGATTCATGAGATTTAGACGCGAGAAATGTTTTGTAAAG 2902
 QY 2328 AAAACATGTGAGAAATAGCAGACTTGGACTGCGCAGAGATATCAACATATAGACT 2387
 DB 2903 AAAACATGTGAGAAATAGCAGACTTGGACTGCGCAGAGATATCAACATATAGACT 2962
 QY 2388 ATTACAAAAGAACCAACATGAGCGGCTTCCAGTCAAGTGAAGGCTCCAGAACCCCTGT 2447
 DB 2963 ATTACAAAAGAACCAACATGAGCGGCTTCCAGTCAAGTGAAGGCTCCAGAACCCCTGT 3022
 QY 2448 TTGATAGAGTATCACTCATCAAGATGTCTGTCTTCCGGGGTGTATATGTGGAGAA 2507
 DB 3023 TTGATAGAGTATCACTCATCAAGATGTCTGTCTTCCGGGGTGTATATGTGGAGAA 3082
 QY 2508 TCTTCCTTAAGGGGGCTGCGCTACACAGAGATTCGCGGAGAGAACTTTTAAGCTGC 2567
 DB 3083 TCTTCCTTAAGGGGGCTGCGCTACACAGAGATTCGCGGAGAGAACTTTTAAGCTGC 3142

QY 2568 TGAAGAGAGACACAGATGATTAAGCCAGCACTGACCAACGAACTGTACATGATGA 2627
 DB 3143 TGAAGAGAGACACAGATGATTAAGCCAGCACTGACCAACGAACTGTACATGATGA 3202
 QY 2628 TGAAGAGACTGTGGCAGTACAGTGGCTTCCAGAGACCAAGCTTCAACAGTGTGTAAAG 2687
 DB 3203 TGAAGAGACTGTGGCAGTACAGTGGCTTCCAGAGACCAAGCTTCAACAGTGTGTAAAG 3262
 QY 2688 ACTTGATGAAATTCATCTCTCAACCAATG----- 2720
 DB 3263 ACTTGATGAAATTCATCTCTCAACCAATGAGAAATCTTGAACCTCAGTCAAGCTTC 3322
 QY 2721 ----- 2720
 DB 3323 TCGAACGATATTCACCTTGTATCTCTGACCAACGATGAATTAACGCTCTCTCCCTT 3382
 QY 2721 -----AGGAATACCTTGGACCTCAGCCAACTCTGAAACGATATTCACCTTACCTTGA 2775
 DB 3383 CTTTCAGGAATATCTTGGACCTCAGCCAACTCTGAAACGATATTCACCTTACCTTGA 3442
 QY 2776 CACAAGAAATCTTGTCTTCAAGAGATGATTTCTTTCTTCTCAACACCCATGCCCTTA 2835
 DB 3443 CACAAGAAATCTTGTCTTCAAGAGATGATTTCTTTCTTCTCAACACCCATGCCCTTA 3502
 QY 2836 CGAACCAATGCTTCTCAGTATCCACATTAAGGGAGTTTAAACATGATGATCTGT 2895
 DB 3503 CGAACCAATGCTTCTCAGTATCCACATTAAGGGAGTTTAAACATGATGATCTGT 3562
 QY 2896 GTCTGCTGCTCCCAACAGAGACAGCACTGAGAACTTATGATACAGAGAGAGACCA 2955
 DB 3563 GTCTGCTGCTCCCAACAGAGACAGCACTGAGAACTTATGATACAGAGAGAGACCA 3622
 QY 2956 TGCCTCCAGAGCTTGTGTCTTCACTTGTATATATGATACAGAGAGTAAATATTTGA 3015
 DB 3623 TGCCTCCAGAGCTTGTGTCTTCACTTGTATATATGATACAGAGAGTAAATATTTGA 3682
 QY 3016 AAGATTAACAGATATGATTAAGTAAAGTATATCAAGTAAACCTGTATCTTCCAGGA 3075
 DB 3683 AAGATTAACAGATATGATTAAGTAAAGTATATCAAGTAAACCTGTATCTTCCAGGA 3742
 QY 3076 GGAGAGAAAGTTTCTGAGAGAGTGAAGCTGC 3106
 DB 3743 GGAGAGAAAGTTTCTGAGAGAGTGAAGCTGC 3773

RESULT 11
 US-10-669-920-600
 ; Sequence 600, Application US/10669920
 ; Publication No. US20060194265A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Moritz, David W.
 ; APPLICANT: Malandro, Marc S.
 ; TITLE OF INVENTION: NOVEL THERAPEUTIC TARGETS IN CANCER
 ; FILE REFERENCE: 20366-066001
 ; CURRENT APPLICATION NUMBER: US/10/669,920
 ; CURRENT FILING DATE: 2003-09-23
 ; PRIOR APPLICATION NUMBER: US 10/004,113
 ; PRIOR FILING DATE: 2001-10-23
 ; PRIOR APPLICATION NUMBER: US 10/052,482
 ; PRIOR FILING DATE: 2001-11-08
 ; PRIOR APPLICATION NUMBER: US 09/997,722
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 ; PRIOR FILING DATE: 2002-03-01
 ; PRIOR APPLICATION NUMBER: US 10/322,281
 ; PRIOR FILING DATE: 2002-12-17
 ; PRIOR APPLICATION NUMBER: US 10/322,696
 ; PRIOR FILING DATE: 2002-12-17
 ; NUMBER OF SEQ ID NOS: 1441

Db	938	GTGTGAGAGATTGGAGTTTAACTGCCAATGGAATTTGAAAGGACCGGGGATTTGTATCCG	997
OY	414	TAAACATAGTCAAGCTGGGGGTCGTTTCATCTGCCTGATCGTGTATCAACATGGCAACTTGT	473
Db	998	TAACTAATGATCAAGCTGGGGGTCGTTTCATCTGCCTGATCGTGTATCAACATGGCAACTTGT	1057
OY	474	CCCTGCGCCGGCCCTCTTCAAGTTTAAAGTATGAGATACCAATTGAGCCAGAAAGCCAC	533
Db	1058	CCCTGCGCCGGCCCTCTTCAAGTTTAAAGTATGAGATACCAATTGAGCCAGAAAGCCAC	1117
OY	534	CAACCAATATCCAAATCTCTTCAACCAAGAATGTAATGAGCTGCGCCAGGGGATCTGCTAG	593
Db	1118	CAACCAATATCCAAATCTCTTCAACCAAGAATGTAATGAGCTGCGCCAGGGGATCTGCTAG	1177
OY	594	AGGTGCGCTGCTGTGTGAAAGATGCGCCGCGATCAAGTGGACTTAAGATGGGTGCACT	653
Db	1178	AGGTGCGCTGCTGTGTGAAAGATGCGCCGCGATCAAGTGGACTTAAGATGGGTGCACT	1237
OY	654	TGGGGCCCAACAAATAGACAGTGTCTTATTTGGGGAGTACTTGACAGATAAAGGCCCAAC	713
Db	1238	TGGGGCCCAACAAATAGACAGTGTCTTATTTGGGGAGTACTTGACAGATAAAGGCCCAAC	1297
OY	714	CTAAGACTCCGGCCTCTATGCTTGTACTGCCAAGTAGACTGTAGACATGTAACCTTGGT	773
Db	1298	CTAAGACTCCGGCCTCTATGCTTGTACTGCCAAGTAGACTGTAGACATGTAACCTTGGT	1357
OY	774	ACTTCATGATGTAATGTCACAGATGCAATCTCATCCGAGATGATGAGGATGACCGAGT	833
Db	1358	ACTTCATGATGTAATGTCACAGATGCAATCTCATCCGAGATGATGAGGATGACCGAGT	1417
OY	834	GTGCGGAAGATTTTGTCTAGTAGAACAAGTAAACAAGAAGACAACATCTGAGCAACA	893
Db	1418	GTGCGGAAGATTTTGTCTAGTAGAACAAGTAAACAAGAAGACAACATCTGAGCAACA	1477
OY	894	CAGAAAGATGAAAAGCGGCTCCATGCTGTGCTGCGGCCAACACTGTCAAGTTTGCT	953
Db	1478	CAGAAAGATGAAAAGCGGCTCCATGCTGTGCTGCGGCCAACACTGTCAAGTTTGCT	1537
OY	954	GCCCAACCGGGGGGAAACCAATGCAACAAGCGGTGCTGAAAAAGGGGAAGATTTA	1013
Db	1538	GCCCAACCGGGGGGAAACCAATGCAACAAGCGGTGCTGAAAAAGGGGAAGATTTA	1597
OY	1014	AGCAGAGACATCGCAATTGAGAGCTTCAAGATACGAACCAACACTGAGCCTCATTAATG	1073
Db	1598	AGCAGAGACATCGCAATTGAGAGCTTCAAGATACGAACCAACAACACTGAGCCTCATTAATG	1657
OY	1074	AAAGTGTGTCCTCATCTGACAAGGAAATTATCCTGTGTAGTGAAGATGATACGGGT	1133
Db	1658	AAAGTGTGTCCTCATCTGACAAGGAAATTATCCTGTGTGTAGTGAAGATGATACGGGT	1717
OY	1134	CCATCAATCAACAGTACCACTTGATGTTGTGAGACCATTCGCCCTCACCGGCCCATCTCC	1193
Db	1718	CCATCAATCAACAGTACCACTTGATGTTGTGAGACCATTCGCCCTCACCGGCCCATCTCC	1777
OY	1194	AAGCCGAGCTGCCGCAAAATGCTTCAAGTGTGCGAGAGAGAGTAGAGTTTGTCTGCA	1253
Db	1778	AAGCCGAGCTGCCGCAAAATGCTTCAAGTGTGCGAGAGAGAGTAGAGTTTGTCTGCA	1837
OY	1254	AGGTTTACAGTATGCCAGGCCCAATCAAGTGTATCAAGCACTGTGAAAAAAGACGGCA	1313
Db	1838	AGGTTTACAGTATGCCAGGCCCAATCAAGTGTATCAAGCACTGTGAAAAAAGACGGCA	1897
OY	1314	GTAATAATACGGGCGCGAGCGGCTGCCCTTCAAGTTCCTCAAGTTCCTCAAGCACTGCCGGATTAATA	1373
Db	1898	GTAATAATACGGGCGCGAGCGGCTGCCCTTCAAGTTCCTCAAGTTCCTCAAGTTCCTGAGCGCGG	1957
OY	1374	GTTCCAAATGCA-----GAAGTGTGCTGCTGTTCATATGACCGAGGCGGA	1419
Db	1958	TGTTAAACACAGGCAAAAGATTTGAGTTCTCTATTTTGGGAATGTAATTTTGGAGA	2017
OY	1420	TGCTGGGGAATATATATGTAAAGTTCCTCAATTTATATAGGAGCGCAACAGTCTGCTG	1479

Db	2018	CGCTGGGGAAATATACGCTGTTGGGGGGTAATTCTAATTGGGATATCTTTCACTCTGCATG	2077
Qy	1480	GCTCACTGTCCTGCGAAACACGACGCGCTGGAGGAAAGAAAGATTTACGTTTCCC	1539
Db	2078	GTTCACAGTTCTGCG-----AGGGCCGTGGAAGAAAGAAAGATTTACGTTTCCC	2128
Qy	1540	AGACTTACTGAGATAGCATCCATTATCTGCAATPAGGGGTCCTTCTTAATGGCCTGTAATGGT	1599
Db	2129	AGACTTACTGAGATAGCATTTTATCTGCATPAGGGGTCCTTCTTAATGGCCTGTAATGGT	2188
Qy	1600	AACAGTCATCTGTGGCGGAATGAAAGAACGACCAAGAACGACAGCTTACAGCAGCCAGCC	1659
Db	2189	AACAGTCATCTGTGGCGGAATGAAAGAACGACCAAGAACGACAGCTTACAGCAGCCAGCC	2248
Qy	1660	GGCTGTGCACAAGCTGACCAAAACGTATCCCTCTGCGAGACAGGTAAACGTTTCGCTGA	1719
Db	2249	GGCTGTGCACAAGCTGACCAAAACGTATCCCTCTGCGAGACAG-----GTTTCGCGTGA	2302
Qy	1720	GTCACAGCTCTCTCATGAACTTCCACACCCCGCTGCTGATGATTAACAACGCGCTCTCTC	1779
Db	2303	GTCACAGCTCTCTCCATGAACTTCCACACCCCGCTGCTGATGATTAACAACGCGCTCTCTC	2362
Qy	1780	AACGGCAGACACCCCGCAATGCTGGAGGGGTCTCCGATATGAATTTCACAGAGACCCAAA	1839
Db	2363	AACGGCAGACACCCCGCAATGCTGGAGGGGTCTCCGATATGAATTTCACAGAGACCCAAA	2422
Qy	1840	ATGGGAGTTTCCAGAGATTAAGCTGACATGGGCAAGCCCTCTGGAGAAAGTTGCTTTGG	1899
Db	2423	ATGGGAGTTTCCAGAGATTAAGCTGACATGGGCAAGCCCTCTGGAGAAAGTTGCTTTGG	2482
Qy	1900	GCAAGTGTCAATGCGCGAAGCATGCGGAATTGACAAAGACAAAGCCCAAGAGGGGGTCAAC	1959
Db	2483	GCAAGTGTCAATGCGCGAAGCATGCGGAATTGACAAAGACAAAGCCCAAGAGGGGGTCAAC	2542
Qy	1960	CGTGGCGGTGAAGATGTTGAAAGATGATGACACAGAGAAAGACCTTTCTGATCTGTGTC	2019
Db	2543	CGTGGCGGTGAAGATGTTGAAAGATGATGACACAGAGAAAGACCTTTCTGATCTGTGTC	2602
Qy	2020	AGAGATGAGATGATGAAAGATGATGGGAAACACAAAGATATCATTAATCTTCTTGAGC	2079
Db	2603	AGAGATGAGATGATGAAAGATGATGGGAAACACAAAGATATCATTAATCTTCTTGAGC	2662
Qy	2080	CTGCACACAGATGGGCTCTTATGTTCATATGTTGATATGCTCTTAAGGCAACTTCCG	2139
Db	2663	CTGCACACAGATGGGCTCTTATGTTCATATGTTGATATGCTCTTAAGGCAACTTCCG	2722
Qy	2140	AGATTAACCTCGAAGCCCGGAGGCCACCCGGGATGGAATGATCTCTATGCAATTAACGCGT	2199
Db	2723	AGATTAACCTCGAAGCCCGGAGGCCACCCGGGATGGAATGATCTCTATGCAATTAACGCGT	2782
Qy	2200	TCTGAGAGAGACATGACCTTCAAGGACTTGTGTGATGCACTTACCAAGCTGGCCAGACG	2259
Db	2783	TCTGAGAGAGACATGACCTTCAAGGACTTGTGTGATGCACTTACCAAGCTGGCCAGACG	2842
Qy	2260	GATGAGATCTTGCGCTTCCAAAATGTATTCATCGAGATTTAGCAGCCAGAAATGTTTT	2319
Db	2843	CATGAGATCTTGCGCTTCCAAAATGTATTCATCGAGATTTAGCAGCCAGAAATGTTTT	2902
Qy	2320	GATTAACAAAAACAATGTGTAAGAAATATPAGCACTTTGGAATCGCCGAGAGATTAACAA	2379
Db	2903	GATTAACAAAAACAATGTGTAAGAAATATPAGCACTTTGGAATCGCCGAGAGATTAACAA	2962
Qy	2380	TATAGACATTAATACAAAAAGAACCAACAATGGCGGCTTCACTCAAGTGAATGGCTCCAGA	2439
Db	2963	TATAGACATTAATACAAAAAGAACCAACAATGGCGGCTTCACTCAAGTGAATGGCTCCAGA	3022
Qy	2440	AGCCCTGTTGATAGATATACACTCATCAGAGTGAATGTCTGTCCTTCCGGGCTGTTAAT	2499
Db	3023	AGCCCTGTTGATAGATATACACTCATCAGAGTGAATGTCTGTCCTTCCGGGCTGTTAAT	3082
Qy	2500	GTGGAGATCTTCACTTAAGGGGGCTGGCCCTACCGAGGATTCGCCGAGAGAACTTT	2559
Db	3083	GTGGAGATCTTCACTTAAGGGGGCTGGCCCTACCGAGAGATTCGCCGAGAGAACTTT	3142

QY	2560	TAAAGCTCTGAAGGAAGAGACACAGAAATGGATTAAGCCAGCCAACTGGACCAACAGAACTGTA	26139
Db	3143	TAACTCTGTGAAGGAAGGACACAGAAATGATTAAGCCAGCCAACTGGACCAACAGAACTGTA	3202
QY	2620	CATGATGATGAGGGGACTGTGGCATGACATGCTCCCTCCAGAGACCAAGTTCAAGCAGTT	2679
Db	3203	CATGATGATGAGGGGACTGTGGCATGACATGCTCCCTCCAGAGACCAAGTTCAAGCAGTT	3262
QY	2680	GGTAGAAGACTTGGATGCAATTCTCACTCTTCACAACTAAG-----	2720
Db	3263	GGTAGAAGACTTGGATGCAATTCTCACTCTTCACAACTAAGGAATATCGACTTCAG	3322
QY	2721	-----	2720
Db	3323	TCAGCTCTCGAACCCTGATTACCTTGTATCTCGAACCCAAAGATGAATAAAGCTCTCT	3382
QY	2721	-----AGATATCTTGGAGACTTCAGCCAACTCTCGAACAATTCACCTAGT	2767
Db	3383	CTTCCTCTCTTCAGGAATATCTTGGAGACTTCAGCCAACTCTCGAACAATTCACCTAGT	3442
QY	2768	TACCTTGACACAGAAAGTTCTTGTCTTCAGAGATGATTCTGTTTTTCTCCAGACCC	2827
Db	3443	TACCTTGACACAGAAAGTTCTTGTCTTCAGAGATGATTCTGTTTTTCTCCAGACCC	3502
QY	2828	ATGCCTTACGAAACCATGCTCTCCAGATTCACACAAATTAACGAGATGTTAAACATGA	2887
Db	3503	ATGCCTTACGAAACCATGCTCTCCAGATTCACACAAATTAACGAGATGTTAAACATGA	3562
QY	2888	ATGACTGTGTCTGCTGTCTCCCAACAGAGACGACTGGAACTAGCTACCTAGCAG	2947
Db	3563	ATGACTGTGTCTGCTGTCTCCCAACAGAGACGACTGGAACTAGCTACCTAGCAG	3622
QY	2948	GGAACCATGCTCTCCCAAGCTTGTGTCTCATTGATATATGATACAGAGAGTAA	3007
Db	3623	GGAACCATGCTCTCCCAAGCTTGTGTCTCATTGATATATGATACAGAGAGTAA	3682
QY	3008	TAATGGAAAAGTATTCAGCATATGTGTAAGATTATACAGTTGAAACTGTATCTT	3067
Db	3683	TAATGGAAAAGTATTCAGCATATGTGTAAGATTATACAGTTGAAACTGTATCTT	3742
QY	3068	CCCCAGAGAGAGAGAGGTTTCTGAGCACTGAGCTGC	3106
Db	3743	CCCCAGAGAGAGAGAGGTTTCTGAGCACTGAGCTGC	3781
RESULT 13			
; US-10-669-920-602			
; Sequence 602, Application US/10669920			
; Publication No. US20060194265A1			
GENERAL INFORMATION:			
APPLICANT: Morris, David W.			
TITLE OF INVENTION: NOVEL THERAPEUTIC TARGETS IN CANCER			
FILE REFERENCE: 20366-066001			
CURRENT APPLICATION NUMBER: US/10/669, 920			
CURRENT FILING DATE: 2003-09-23			
PRIOR APPLICATION NUMBER: US 10/004, 113			
PRIOR FILING DATE: 2001-10-23			
PRIOR APPLICATION NUMBER: US 10/052, 482			
PRIOR FILING DATE: 2001-11-08			
PRIOR APPLICATION NUMBER: US 09/997, 722			
PRIOR FILING DATE: 2001-11-30			
PRIOR APPLICATION NUMBER: US 10/034, 650			
PRIOR FILING DATE: 2001-12-20			
PRIOR APPLICATION NUMBER: US 10/085, 117			
PRIOR FILING DATE: 2002-02-27			
PRIOR APPLICATION NUMBER: US 10/087, 192			
PRIOR FILING DATE: 2002-03-01			
PRIOR APPLICATION NUMBER: US 10/322, 281			
PRIOR FILING DATE: 2002-12-17			
PRIOR APPLICATION NUMBER: US 10/322, 696			
PRIOR FILING DATE: 2002-12-17			

[illegible]

DB 1087 CAGAAAAGATGAAAAGCGGCTTCATGCTGTGCTTCGCGCAACACTGTCAGATTTCGCT 1146
QY 954 GCCCAGCCGCGGGGGAACCCATGECACCAACATGCGGTGCTGAAAAACGGAAAGAGTTTA 1013
DB 1147 GCCCAGCCGCGGGGGAACCCATGECACCAACATGCGGTGCTGAAAAACGGAAAGAGTTTA 1206
QY 1014 AGCAGAGCATGCGATTGAGGCTTACAGATGACGAAACAGCATGAGACCTCATTTATG 1073
DB 1207 ACAGAGAGCATGCGATTGAGGCTTACAGATGACGAAACAGCATGAGACCTCATTTATG 1266
QY 1074 AAGGTGTGCTCCATCTGACAAAGGAAATTTATACCTGTAGTGAAGATGATACGGGT 1133
DB 1267 AAGGTGTGCTCCATCTGACAAAGGAAATTTATACCTGTGTGAGATGATACGGGT 1326
QY 1134 CCATCAATCAACGTAACCACTGATGTTGTGAGGATCGCTCAACCGGACCATCTCC 1193
DB 1327 CCATCAATCAACGTAACCACTGATGTTGTGAGGATCGCTCAACCGGACCATCTCC 1386
QY 1194 AAGCGGACTGCGCGCAATGCTTCCACAGTGTGCGAGAGACGTAAGTTTGTCTGCA 1253
DB 1387 AAGCGGACTGCGCGCAATGCTTCCACAGTGTGCGAGAGACGTAAGTTTGTCTGCA 1446
QY 1254 AAGTTTACGATGATGCGCGACCCCAATCAGTGAATCAAGACGTAAGAAAGAACGCA 1313
DB 1447 AAGTTTACGATGATGCGCGACCCCAATCAGTGAATCAAGACGTAAGAAAGAACGCA 1506
QY 1314 GTAAATACGGGCGCGACGCGGCTGCTCACTCAAGTTCTCAAGCACTCGGGATTAATA 1373
DB 1507 GTAAATACGGGCGCGACGCGGCTGCTCACTCAAGTTCTCAAGCACTCGGGATTAATA 1566
QY 1374 GTTCCATGCAAGAGTGTGCTCTGTCAATGTGACCGAGCGGATGCTGGGAAATATA 1433
DB 1567 GTTCCATGCAAGAGTGTGCTCTGTCAATGTGACCGAGCGGATGCTGGGAAATATA 1626
QY 1434 TATGTAGGCTTCCATTTATATAGGCGAGGCAACAGCTGCGTGGCTCACTGTCTGCG 1493
DB 1627 TATGTAGGCTTCCATTTATATAGGCGAGGCAACAGCTGCGTGGCTCACTGTCTGCG 1686
QY 1494 CAAAACAGCAAGCGCTGGAAGAAAGAAATTAACGCTTCCCACTCACTGAGAGA 1553
DB 1687 CAAAACAGCAAGCGCTGGAAGAAAGAAATTAACGCTTCCCACTCACTGAGAGA 1746
QY 1554 TAGCCATTTACTGATAGGCGGTCTTCTTATGCTGCTGTATGCTGTAACTGATCTGT 1613
DB 1747 TAGCCATTTACTGATAGGCGGTCTTCTTATGCTGCTGTATGCTGTAACTGATCTGT 1806
QY 1614 GCGGATGAAAGAACAGCAACAGAAAGCACTTTCAGCGAGCCGCGCTGTGCAACAGC 1673
DB 1807 GCGGATGAAAGAACAGCAACAGAAAGCACTTTCAGCGAGCCGCGCTGTGCAACAGC 1866
QY 1674 TGACCAAAAGTATCCCTGTCGCGAGACAGGTAAAC---AGTTTCGCTGATGCTCAGCTCC 1729
DB 1867 TGACCAAAAGTATCCCTGTCGCGAGACAGGTAAACAAAGTTTCGCTGATGCTCAGCTCC 1926
QY 1730 TCCATGAACTCCAAACACCCGCTGTGTGAGATTAACAACGCTCTCTTCAACGCGAGAC 1789
DB 1927 TCCATGAACTCCAAACACCCGCTGTGTGAGATTAACAACGCTCTCTTCAACGCGAGAC 1986
QY 1790 ACCCCCATGCTGCGAGGCGTCTCCGAGTAACTTCCAGAGGACCCAAAGAGGAGTTT 1849
DB 1987 ACCCCCATGCTGCGAGGCGTCTCCGAGTAACTTCCAGAGGACCCAAAGAGGAGTTT 2046
QY 1850 CCAAGAGATGAGTGAACCTGCGCAAGCCCTGCGAGAGAGTTGCTTGGCGCAAGTGTCT 1909
DB 2047 CCAAGAGATGAGTGAACCTGCGCAAGCCCTGCGAGAGAGTTGCTTGGCGCAAGTGTCT 2106
QY 1910 ATGGCGAAAGCACTGGGAATTGACAAAGACAGCCCAAGAGGCGGTCACTGCGCGGTG 1969
DB 2107 ATGGCGAAAGCACTGGGAATTGACAAAGACAGCCCAAGAGGCGGTCACTGCGCGGTG 2166
QY 1970 AAGATTTAAAGATGATGCAAGAGAAAGACCTTCTGATGTGCTCAAGATGAG 2029

DB 2167 AAGATTTAAAGATGATGCAAGAGAAAGACCTTCTGATCTGTGTCAAGATGAG 2226
QY 2030 ATGATGAAGATGATTGGGAAACACAGAAATATATATTTCTTTGGAGCCCTGCAACAG 2089
DB 2227 ATGATGAAGATGATTGGGAAACACAGAAATATATATTTCTTTGGAGCCCTGCAACAG 2286
QY 2090 GATGGGCTCTCTATGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2149
DB 2287 GATGGGCTCTCTATGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2346
QY 2150 CGAGCCCGAGGCGCACCCGGAATGAGATCTCTTAATGACATTAACGTTTCTGAGAG 2209
DB 2347 CGAGCCCGAGGCGCACCCGGAATGAGATCTCTTAATGACATTAACGTTTCTGAGAG 2406
QY 2210 CAGATGACCTTCAAGGACTTGTGTGATGATGATGATGATGATGATGATGATGATGAT 2269
DB 2407 CAGATGACCTTCAAGGACTTGTGTGATGATGATGATGATGATGATGATGATGATGAT 2466
QY 2270 TTGGCTTCCAAAATGATTCATGAGATTTAGGAGCGAGAAATGTTTGGTAAACAG 2329
DB 2467 TTGGCTTCCAAAATGATTCATGAGATTTAGGAGCGAGAAATGTTTGGTAAACAG 2526
QY 2330 AACATGTGATGATAAATAGCAGACTTGTGACTGCGCAGAGATATCAACATATAGACTAT 2389
DB 2527 AACATGTGATGATAAATAGCAGACTTGTGACTGCGCAGAGATATCAACATATAGACTAT 2586
QY 2390 TACAAAAGACCAACAAATGCGGCGCTTCAGTCAAGTGAATGCTCCAGAAAGCCCTGTT 2449
DB 2587 TACAAAAGACCAACAAATGCGGCGCTTCAGTCAAGTGAATGCTCCAGAAAGCCCTGTT 2646
QY 2450 GATAGATATACATCAATCAGATGATGATGATGATGATGATGATGATGATGATGATGAT 2509
DB 2647 GATAGATATACATCAATCAGATGATGATGATGATGATGATGATGATGATGATGATGAT 2706
QY 2510 TTCACTTTAGGCGGCTGCGCTTACCCAGAGATTCCTGTAAGAGAACTTTTAAGTCTG 2569
DB 2707 TTCACTTTAGGCGGCTGCGCTTACCCAGAGATTCCTGTAAGAGAACTTTTAAGTCTG 2766
QY 2570 AAGAAAGACACAGAAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2629
DB 2767 AAGAAAGACACAGAAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2826
QY 2630 AGGAGCTGTGGCAAGAGTGCCTCCAGAGACCAAGTTCAGAGTGTGTAGAGAGC 2689
DB 2827 AGGAGCTGTGGCAAGAGTGCCTCCAGAGACCAAGTTCAGAGTGTGTAGAGAGC 2886
QY 2690 TTGATGCAATTTCACTCTCAACCAATGAG 2722
DB 2887 TTGATGCAATTTCACTCTCAACCAATGAG 2919

RESULT 14
US-10-669-920-626
Sequence 626, Application US/10669920
Publication No. US20060194265A1
GENERAL INFORMATION:
APPLICANT: Morris, David W.
APPLICANT: Malandro, Marc S.
TITLE OF INVENTION: NOVEL THERAPEUTIC TARGETS IN CANCER
FILE REFERENCE: 20366-066001
CURRENT APPLICATION NUMBER: US/10/669,920
CURRENT FILING DATE: 2003-09-23
PRIOR APPLICATION NUMBER: US 10/004,113
PRIOR FILING DATE: 2001-10-23
PRIOR APPLICATION NUMBER: US 10/052,482
PRIOR FILING DATE: 2001-11-08
PRIOR APPLICATION NUMBER: US 09/997,722
PRIOR FILING DATE: 2001-11-30
PRIOR APPLICATION NUMBER: US 10/034,650
PRIOR FILING DATE: 2001-12-20
PRIOR APPLICATION NUMBER: US 10/085,117
PRIOR FILING DATE: 2002-02-27
PRIOR APPLICATION NUMBER: US 10/087,192

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; PRIOR FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 10/322,281
; PRIOR FILING DATE: 2002-12-17
; PRIOR APPLICATION NUMBER: US 10/322,696
; PRIOR FILING DATE: 2002-12-17
; NUMBER OF SEQ ID NOS: 1441
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 626
; LENGTH: 3632
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-669-920-626

Query Match      85.0%; Score 2641.4; DB 6; Length 3632;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 2716; Conservative 0; Mismatches 6; Indels 11; Gaps 6;

QY 1 CCCCAGACAAAGTTGGTGGAGGCAAG-CAAGCTAGTCCTTTCTTCCTCGTTCC 59
DB CTCGAGACAAAGTTGGTGGAGGCAAGCCAAAGCTAGTCCTTTCTTCCTCGTTCC 637
QY 60 CCAATCCGAGGAGGAGCCCGCGGCGGTATG---GCGCTCTCCGACGCTGGGTAGCG 116
DB CCAATCCGAGGAGGAGCCCGCGGCGGTATGCGCGCGCTCTCCGACGCTGGGTAGCG 697
QY 117 GTGAAGCCCGGAGGCTTGGCGCGCGGCAAGACCAAGAGCACTTCTGCGTTGAG 176
DB GTGAAGCCCGGAGGCTTGGCGCGCGGCAAGACCAAGAGCACTTCTGCGTTGAG 757
QY 177 TTGCTCCCGGACCCCGGCGTGGTGGCTTCTCATCCGACCGAGCGGGGCG-CGGG 235
DB TTGCTCCCGGACCCCGGCGTGGTGGCTTCTCATCCGACCGAGCGGGGCGCGGG 817
QY 758 TTGCTCCCGGACCCCGGCGTGGTGGCTTCTCATCCGACCGAGCGGGGCGCGGG 817
DB TTGCTCCCGGACCCCGGCGTGGTGGCTTCTCATCCGACCGAGCGGGGCGCGGG 817
QY 226 ACAACAGAGTGGCGGAGGAGGCTTGCATTCAAGTGACTGAGAGGAGC-GCAGCGC 294
DB ACAACAGAGTGGCGGAGGAGGCTTGCATTCAAGTGACTGAGAGGAGCAGCGCGC 877
QY 235 TCGGTTCTGAGCCCAACGCA-GCTGAAGGCAATTGGCGGTAGTCCATGCGGTAGAG 353
DB TCGGTTCTGAGCCCAACGCAAGGCTGAAGGCAATTGGCGGTAGTCCATGCGGTAGAG 937
QY 334 GTGTGCAATGGGATTTAAGTCCATGAGATATGGAAGAGAGACCGGGGATTTGTA 413
DB GTGTGCAATGGGATTTAAGTCCATGAGATATGGAAGAGAGACCGGGGATTTGTA 997
QY 938 GTGTGCAATGGGATTTAAGTCCATGAGATATGGAAGAGAGACCGGGGATTTGTA 997
DB TAAACATGAGTCAAGTGGGTCGTTTCATGCTGGTCAACATGAGCAACCTTGT 473
QY 414 TAAACATGAGTCAAGTGGGTCGTTTCATGCTGGTCAACATGAGCAACCTTGT 473
DB TAAACATGAGTCAAGTGGGTCGTTTCATGCTGGTCAACATGAGCAACCTTGT 1057
QY 474 CCTGGCCCGGCTCTCTTCAGTTTAGTTAGAGATACCAATTAGAGCCAGAGCCAC 533
DB CCTGGCCCGGCTCTCTTCAGTTTAGTTAGAGATACCAATTAGAGCCAGAGCCAC 1117
QY 534 CAACCAAAATCAAAATCTCAACCAAGAGTGAAGTGGCTGGCCAGGGGAGTGGCTAG 593
DB CAACCAAAATCAAAATCTCAACCAAGAGTGAAGTGGCTGGCCAGGGGAGTGGCTAG 1177
QY 1118 CAACCAAAATCAAAATCTCAACCAAGAGTGAAGTGGCTGGCCAGGGGAGTGGCTAG 1177
DB AGGTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCT 653
QY 594 AGGTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCT 653
DB AGGTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCT 1237
QY 1178 AGGTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCT 1237
DB TGGGGCCCAACATAGAGAGAGTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCT 713
QY 654 TGGGGCCCAACATAGAGAGAGTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCT 713
DB TGGGGCCCAACATAGAGAGAGTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCT 1297
QY 714 CTAGAGACTCCGGCTCTTATGCTTGAATGCGCACTGAGAGCACTGAGAACTTGGT 773
DB CTAGAGACTCCGGCTCTTATGCTTGAATGCGCACTGAGAGCACTGAGAACTTGGT 1357
QY 1298 CTAGAGACTCCGGCTCTTATGCTTGAATGCGCACTGAGAGCACTGAGAACTTGGT 1357
DB ACTTCATGAGTGAATGTCAGAGATGCACTCACTCCGAGATGATGAGATGACACCGATG 833
QY 774 ACTTCATGAGTGAATGTCAGAGATGCACTCACTCCGAGATGATGAGATGACACCGATG 833
DB ACTTCATGAGTGAATGTCAGAGATGCACTCACTCCGAGATGATGAGATGACACCGATG 1417
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QY 834 GTGGGAAGATTTTGTGATGAGAGCAAGTAAACAAGAGGACCATCTGAGCCAA 893
DB GTGGGAAGATTTTGTGATGAGAGCAAGTAAACAAGAGGACCATCTGAGCCAA 1477
QY 894 CAGAAAAGATGAAAAGCGGCTCCATGCTGTGCTGGGCAACACTGTCAAGTTTGGT 953
DB CAGAAAAGATGAAAAGCGGCTCCATGCTGTGCTGGGCAACACTGTCAAGTTTGGT 1537
QY 954 GCCAGCGGGGGGAGACCCCAATGCAACATGCGGTGGCTGAAAAGCGGAAGATTTA 1013
DB GCCAGCGGGGGGAGACCCCAATGCAACATGCGGTGGCTGAAAAGCGGAAGATTTA 1597
QY 1014 AGCAGAGCATTCGATTTGAGGCTACAGAGTACAGAACTGAGGCTCTATATGG 1073
DB AGCAGAGCATTCGATTTGAGGCTACAGAGTACAGAACTGAGGCTCTATATGG 1657
QY 1598 AGCAGAGCATTCGATTTGAGGCTACAGAGTACAGAACTGAGGCTCTATATGG 1657
DB AAGGTGTGCTCCATCTGACAGGGAATATATACCTGTGTATGAGAAATGATACGGGT 1133
QY 1074 AAGGTGTGCTCCATCTGACAGGGAATATATACCTGTGTATGAGAAATGATACGGGT 1133
DB AAGGTGTGCTCCATCTGACAGGGAATATATACCTGTGTATGAGAAATGATACGGGT 1717
QY 1658 AAGGTGTGCTCCATCTGACAGGGAATATATACCTGTGTATGAGAAATGATACGGGT 1717
DB CCATCATCAGAGTACCTGATATGTTGAGAGCGATGCGCTCACCGGCCATCTCTCC 1193
QY 1134 CCATCATCAGAGTACCTGATATGTTGAGAGCGATGCGCTCACCGGCCATCTCTCC 1193
DB CCATCATCAGAGTACCTGATATGTTGAGAGCGATGCGCTCACCGGCCATCTCTCC 1777
QY 1194 AAGCGGAGCTGGCGGCAAAATGCTTCAAGTGTGCGAGAGAGAGCTAGAGTTTGTGCA 1253
DB AAGCGGAGCTGGCGGCAAAATGCTTCAAGTGTGCGAGAGAGAGCTAGAGTTTGTGCA 1837
QY 1778 AAGCGGAGCTGGCGGCAAAATGCTTCAAGTGTGCGAGAGAGAGCTAGAGTTTGTGCA 1837
DB AAGTTTACAGTATGCCAGCCCAATCCATCCAGTGTATCAAGCACTGGGGAATATA 1313
QY 1254 AAGTTTACAGTATGCCAGCCCAATCCATCCAGTGTATCAAGCACTGGGGAATATA 1313
DB AAGTTTACAGTATGCCAGCCCAATCCATCCAGTGTATCAAGCACTGGGGAATATA 1897
QY 1898 AAGTTTACAGTATGCCAGCCCAATCCATCCAGTGTATCAAGCACTGGGGAATATA 1957
DB AAGTTTACAGTATGCCAGCCCAATCCATCCAGTGTATCAAGCACTGGGGAATATA 1957
QY 1314 GTAAATATAGGAGCCGAGGAGTGGCTTCAAGTGTATCAAGCACTGGGGAATATA 1373
DB GTAAATATAGGAGCCGAGGAGTGGCTTCAAGTGTATCAAGCACTGGGGAATATA 1957
QY 1374 GTTCCAAATGAGAGTGTGCTGCTCAATGATGACAGAGCGGATGCTGGGGAATATA 1433
DB GTTCCAAATGAGAGTGTGCTGCTCAATGATGACAGAGCGGATGCTGGGGAATATA 2017
QY 1958 GTTCCAAATGAGAGTGTGCTGCTCAATGATGACAGAGCGGATGCTGGGGAATATA 2017
DB TATGTAAAGTCTCCAAATATATAGGAGGAGGCAACAGTGTGCTGCTGCTGCTGCTG 2077
QY 1434 TATGTAAAGTCTCCAAATATATAGGAGGAGGCAACAGTGTGCTGCTGCTGCTGCTG 1493
DB TATGTAAAGTCTCCAAATATATAGGAGGAGGCAACAGTGTGCTGCTGCTGCTGCTG 2077
QY 1494 CAATAACAGAAAGCGCTTGAAGAGAGAGATTAAGCTTCCCAAGACTACCTGGAGA 1553
DB CAATAACAGAAAGCGCTTGAAGAGAGAGATTAAGCTTCCCAAGACTACCTGGAGA 2137
QY 2078 CAATAACAGAAAGCGCTTGAAGAGAGAGATTAAGCTTCCCAAGACTACCTGGAGA 2137
DB TAGCCATTATCTGATAGGAGGCTTCTTAATGCTGTATGATGATGATGATGATGATG 1613
QY 1554 TAGCCATTATCTGATAGGAGGCTTCTTAATGCTGTATGATGATGATGATGATGATG 1613
DB TAGCCATTATCTGATAGGAGGCTTCTTAATGCTGTATGATGATGATGATGATGATG 2197
QY 1614 GCCGAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1673
DB GCCGAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2257
QY 2198 GCCGAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2257
DB TGAACCAAAAGTATCCCTGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2317
QY 2258 TGAACCAAAAGTATCCCTGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2317
DB TCCATGAATCTCAACACCCGCTGTGTAGAGATTAACACACGCTCTCTTCAACGAGAG 2377
QY 1730 TCCATGAATCTCAACACCCGCTGTGTAGAGATTAACACACGCTCTCTTCAACGAGAG 1789
DB ACCCCATGCTGGCAGGAGGCTCTCCAGATATGAATCTTCAAGAGAGCCAAATAGGAGTTT 1849
QY 1790 ACCCCATGCTGGCAGGAGGCTCTCCAGATATGAATCTTCAAGAGAGCCAAATAGGAGTTT 1849
DB ACCCCATGCTGGCAGGAGGCTCTCCAGATATGAATCTTCAAGAGAGCCAAATAGGAGTTT 2437
QY 2378 ACCCCATGCTGGCAGGAGGCTCTCCAGATATGAATCTTCAAGAGAGCCAAATAGGAGTTT 2437
DB CCAAGAGATAGCTGACACTGGGCAAGCCCTGCGGAGAGAGAGTTGTTGGGCAATGGTGC 1909
QY 1850 CCAAGAGATAGCTGACACTGGGCAAGCCCTGCGGAGAGAGAGTTGTTGGGCAATGGTGC 1909
DB CCAAGAGATAGCTGACACTGGGCAAGCCCTGCGGAGAGAGAGTTGTTGGGCAATGGTGC 2497
QY 2438 CCAAGAGATAGCTGACACTGGGCAAGCCCTGCGGAGAGAGAGTTGTTGGGCAATGGTGC 2497
DB ATGGGGAAGAGAGTGGGAATTGAACAAGCAAGCCCAAGAGAGCGGTCAACGCTGGCGGTG 1969
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Db      2498 ATGGCGAAGCACTGGGAATTGCAAGACAGCCAGAGGCGGTACCGGCGCTG 2557
Qy      1970 AAGATGTGAAAGATGATGCAAGAGAAAGACCTTTGTGATGTGTCAAGATGAG 2029
Db      2558 AAGATGTGAAAGATGATGCAAGAGAAAGACCTTTGTGATGTGTCAAGATGAG 2617
Qy      2030 ATGATGAAGTGTGTTGGGAAACCAAGAAATATATTAATCTTTGGAGCTGCACAG 2089
Db      2618 ATGATGAAGTGTGTTGGGAAACCAAGAAATATATTAATCTTTGGAGCTGCACAG 2677
Qy      2090 GATGGGCTCTCATATGTCATAGTATGATGATGCTTAAAGGCAACTCCGAGATACCTC 2149
Db      2678 GATGGGCTCTCATATGTCATAGTATGATGATGCTTAAAGGCAACTCCGAGATACCTC 2737
Qy      2150 CGAGCCCGAGAGGCAACCCGGGATGAGATACCTCTATGACATTAACCGTGTCTTGAGAG 2209
Db      2738 CGAGCCCGAGAGGCAACCCGGGATGAGATACCTCTATGACATTAACCGTGTCTTGAGAG 2797
Qy      2210 CAGATGACCTTCAAGGACTTGTGTGATGCACTTACAGCTGCGCAGAGATGAGTAC 2269
Db      2798 CAGATGACCTTCAAGGACTTGTGTGATGCACTTACAGCTGCGCAGAGATGAGTAC 2857
Qy      2270 TTGGCTTCCCAAAATGATTCATGAGATTTAGCAAGCCAGAAATGTTTGTGTAACAGAA 2329
Db      2858 TTGGCTTCCCAAAATGATTCATGAGATTTAGCAAGCCAGAAATGTTTGTGTAACAGAA 2917
Qy      2330 AACATGTGATGAAATATAGCAGACTTTGAGACTCGCAGAGATATCAACATATAGACTAT 2389
Db      2918 AACATGTGATGAAATATAGCAGACTTTGAGACTCGCAGAGATATCAACATATAGACTAT 2977
Qy      2390 TACAAAGAACCAACCAATGAGGCGGCTTCCAGTCAAGTGTGCTCCAGAGCCCTGTTT 2449
Db      2978 TACAAAGAACCAACCAATGAGGCGGCTTCCAGTCAAGTGTGCTCCAGAGCCCTGTTT 3037
Qy      2450 GATAGAGTATACCTGATGAGATGATGCTGCTCCGAGGATGTAATGTGGAGATC 2509
Db      3038 GATAGAGTATACCTGATGAGATGATGCTGCTCCGAGGATGTAATGTGGAGATC 3097
Qy      2510 TTCACTTTAGGGGGCTCGCCCTTACCAAGGATTCGGGTGAGAGAACTTTTAAAGCTGCTG 2569
Db      3098 TTCACTTTAGGGGGCTCGCCCTTACCAAGGATTCGGGTGAGAGAACTTTTAAAGCTGCTG 3157
Qy      2570 AAGAGAGACACAGAAATGATTAAGCCAGCACTGCAACCACTGTAATGATGATG 2629
Db      3158 AAGAGAGACACAGAAATGATTAAGCCAGCACTGCAACCACTGTAATGATGATG 3217
Qy      2630 AGGAGCTGTTGGATGAGGCGCTCCAGAGACCAACGTTCAAGCAGTTGTGTAAGAGC 2689
Db      3218 AGGAGCTGTTGGATGAGGCGCTCCAGAGACCAACGTTCAAGCAGTTGTGTAAGAGC 3277
Qy      2690 TTGATGCAATTTCTCACTCTCAACCAATGAG 2722
Db      3278 TTGATGCAATTTCTCACTCTCAACCAATGAG 3310

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RESULT 15

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US-10-669-920-570
; Sequence 570, Application US/10669920
; Publication No. US20060194265A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
; APPLICANT: Malandro, Marc S.
; TITLE OF INVENTION: NOVEL THERAPEUTIC TARGETS IN CANCER
; FILE REFERENCE: 20366-066001
; CURRENT APPLICATION NUMBER: US/10/669,920
; CURRENT FILING DATE: 2003-09-23
; PRIOR APPLICATION NUMBER: US 10/004,113
; PRIOR FILING DATE: 2001-10-23
; PRIOR APPLICATION NUMBER: US 10/052,482
; PRIOR FILING DATE: 2001-11-08
; PRIOR APPLICATION NUMBER: US 09/997,722
; PRIOR FILING DATE: 2001-11-30

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; PRIOR APPLICATION NUMBER: US 10/034,650
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: US 10/085,117
; PRIOR FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: US 10/087,192
; PRIOR FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 10/322,281
; PRIOR FILING DATE: 2002-12-17
; PRIOR APPLICATION NUMBER: US 10/322,696
; PRIOR FILING DATE: 2002-12-17
; NUMBER OF SEQ ID NOS: 1441
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 570
; LENGTH: 3238
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-669-920-570

Query Match      80.7%; Score 2506.2; DB 6; Length 3238;
Best Local Similarity 96.8%; Pred. No. 0;
Matches 2650; Conservative 0; Mismatches 63; Indels 26; Gaps 8;

Qy      1 CCCGAGAGCAAGTTGTGAGAGCAAG-CAAGCTGAGTCTTTCTCTGCTGCTCC 59
Db      187 CTCGGAGCAAGTTGTGAGAGCAAGCAAGCTGAGTCTTTCTCTGCTGCTCC 246
Qy      60 CCAATCCGAGGCGAGCCCGCGGCGTCAAG--GCGCTCTCCGAGCGCTGCGGTACGC 116
Db      247 CCAATCCGAGGCGAGCCCGCGGCGTCAAGCCGCGCTCTCCGAGCGCTGCGGTACGC 306
Qy      117 GTGAAGCCCGGAGGCTTGGCGCGCGAGAGACCAAGAGACCACTTTCTGCGTTTGAAG 176
Db      307 GTGAAGCCCGGAGGCTTGGCGCGCGAGAGACCAAGAGACCACTTTCTGCGTTTGAAG 366
Qy      177 TTGCTCCCGCAACCCCGGCGTGTGCTTTTCCATCCGACCAAGCGGCGGC-CGGG 235
Db      367 TTGCTCCCGCAACCCCGGCGTGTGCTTTTCCATCCGACCAAGCGGCGGC 426
Qy      236 ACAACACAGGTGCGGAGAGAGGCTTCCATTCAGATGATGACAGCAGCAGC-GCAGCGCC 294
Db      427 ACAACACAGGTGCGGAGAGAGGCTTCCATTCAGATGATGACAGCAGCAGCAGCGCC 486
Qy      295 TCGGTTCTGAGCCCAACCGCA-GCTGAAGGATTTGGCGTATGCTATGCCGTAGAGAA 353
Db      487 TCGGTTCTGAGCCCAACCGCAAGCTGAGAGCACTTGGCGTATGCTATGCCGTAGAGAA 546
Qy      354 GTGTGAGATGAGATTAACGTCCACATGAGATATGAAAGAGACCGGGATTTGTACCG 413
Db      547 GTGTGAGATGAGATTAACGTCCACATGAGATATGAAAGAGACCGGGATTTGTACCG 606
Qy      414 TAAACATGATGAGTGGGCTGCTTCACTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 473
Db      607 TAAACATGATGAGTGGGCTGCTTCACTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 666
Qy      474 CCTGGCCCGCGCCCTTCATGTTAGTGAAGATACCAATTAAGCCAGAGAGACCAAC 533
Db      667 CCTGGCCCGCGCCCTTCATGTTAGTGAAGATACCAATTAAGCCAGAGAGACCAAC 726
Qy      534 CAACCAATATACCAAAATCTCTCAACAGAGATACGTGCTGCGCCAGAGAGTGTCTAG 593
Db      727 CAACCAATATACCAAAATCTCTCAACAGAGATACGTGCTGCGCCAGAGAGTGTCTAG 786
Qy      594 AGGTGCGCTGCTGTTGAAAGATGCCCGGTGATCAGTTGACTTAAGATGGGCTGCACT 653
Db      787 AGGTGCGCTGCTGTTGAAAGATGCCCGGTGATCAGTTGACTTAAGATGGGCTGCACT 846
Qy      654 TGGGGCCCAACATATGAGCAGTGTATTTGGGAGATCTTGAAGATTAAGGCGCCACAC 713
Db      847 TGGGGCCCAACATATGAGCAGTGTATTTGGGAGATCTTGAAGATTAAGGCGCCACAC 906
Qy      714 CTAGAGACTCCGCGCTTATGCTTGTATCTGACAGTATGAGACTGTATGAACTTGTGT 773
Db      907 CTAGAGACTCCGCGCTTATGCTTGTATCTGACAGTATGAGACTGTATGAACTTGTGT 966

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QY	774	ACTTCATGCTGAATGTCACAGATGTCATCTCTCAATCCGAGATGATGAGATGACACCGATG	893
Db	967	ACTTCATGCTGAATGTCACAGATGTCATCTCTCAATCCGAGATGATGAGATGACACCGATG	1026
QY	834	GTGGGAAAGATTTTGTCTGATGAGAACAGTAAACAACAAGAGACCATATCTGACCAACA	893
Db	1027	GTGGGAAAGATTTTGTCTGATGAGAACAGTAAACAACAAGAGACCATATCTGACCAACA	1086
QY	894	CAGAAAGATGAAAAGCGGCTCCATGCTGTGCTGCGGCCAACATCTGTCAATTTTGCT	953
Db	1087	CAGAAAGATGAAAAGCGGCTCCATGCTGTGCTGCGGCCAACATCTGTCAATTTTGCT	1146
QY	954	GCCGACCGGGGGGAAACCCATGCGCAACATGCGGTGCTGAAAAAGGAGAGTTTA	1013
Db	1147	GCCGACCGGGGGGAAACCCATGCGCAACATGCGGTGCTGAAAAAGGAGAGTTTA	1206
QY	1014	AGCAGAGCATCGCATTTGAGAGCTTACAAGTATCGAAACACAGCACTGAGCCTCATTTATG	1073
Db	1207	AGCAGAGCATCGCATTTGAGAGCTTACAAGTATCGAAACACAGCACTGAGCCTCATTTATG	1266
QY	1074	AAAGTGTGTCCTCATCTTGAACAAGGAAATTATACCTGTGTATGTGAGAAATGAATACGGT	1133
Db	1267	AAAGTGTGTCCTCATCTTGAACAAGGAAATTATACCTGTGTGTGAGAAATGAATACGGT	1326
QY	1134	CCATCAATCAACAGTACCACTGATGTGTTGAGAGCATTCGCTACCGGCCCATCTCTCC	1193
Db	1327	CCATCAATCAACAGTACCACTGATGTGTTGAGAGCATTCGCTACCGGCCCATCTCTCC	1386
QY	1194	AAAGCCGACTGCGGCGCAATATGCTTCAACATGTGTGAGAGAGATGATTTGTCTGCA	1253
Db	1387	AAAGCCGACTGCGGCGCAATATGCTTCAACATGTGTGAGAGAGATGATTTGTCTGCA	1446
QY	1254	AGGTTTACAGTATGATCCCGACGCCCATCTCAGTGGATCAACAGTGGAAAGAAGACGGCA	1313
Db	1447	AGGTTTACAGTATGATCCCGACGCCCATCTCAGTGGATCAACAGTGGAAAGAAGACGGCA	1506
QY	1314	GTAAATACGGGCGCCGACGGGCTGCTTCACTTCAAGGTTCTCAAGCACTCGGGATTAATA	1373
Db	1507	GTAAATACGGGCGCCGACGGGCTGCTTCACTTCAAGGTTCTCAAGGCGCCCGGTGTAAACA	1566
QY	1374	GTTCCAAATGCAAGATGCTGCGTCTGT-----TCAAATGATCCGAGCGGATGCTGGGG	1427
Db	1567	CCACGACCAAGAGATGATGATGTTCTCTATATTCGGAATGTAACTTTTBAGAACGCTGGGG	1626
QY	1428	AATATATATGTAAAGTCTCTCAATTATATAGGCGACGCCAACAGTCTGCTGACTG	1487
Db	1627	AATATATGCTGTGGCGGGTAAATCTATTTGGGATATCTTTCACTCTGCATGTGTAAG	1686
QY	1488	TCCTGCGCAAAACAGCAGCGGCTGGAAAGAAAGAAATTAACAGCTTCCCAACATACC	1547
Db	1687	TCCTGCG-----AGCGCTGGAAAGAAAGAAAGAAATTAACAGCTTCCCAACATACC	1737
QY	1548	TGGAATATGCACTTACTACTGCAATAGGGGCTTTTATATGCGCTGTATGTGTTAACATCA	1607
Db	1738	TGGAATATGCACTTACTACTGCAATAGGGGCTTTTATATGCGCTGTATGTGTTAACATCA	1797
QY	1608	TCCTGTGCGCAATGAAGACAGACCAAGAACCAAGCTTACGACGCGCGGCTGTGC	1667
Db	1798	TCCTGTGCGCAATGAAGACAGACCAAGAACCAAGCTTACGACGCGCGGCTGTGC	1857
QY	1668	ACAAAGCTGACAAAGATATCCCGCTGCGGAGACAGTAAAC-----AGTTTGGCTGAGTCC	1723
Db	1858	ACAAAGCTGACAAAGATATCCCGCTGCGGAGACAGTAAACAGAAAGTTTCGCTGAGTCC	1917
QY	1724	AGCTCTCATGAACTCCAAACACCCCGCTGTGAGATTAACAACAGGCTCTTTCAACG	1783
Db	1918	AGCTCTCATGAACTCCAAACACCCCGCTGTGAGATTAACAACAGGCTCTTTCAACG	1977
QY	1784	GCAGACACCCCAATGTGCGACAGGGTCTCCAGATATGAATTTCCAGAGAACCAAAATGG	1843
Db	1978	GCAGACACCCCAATGTGCGACAGGGTCTCCAGATATGAATTTCCAGAGAACCAAAATGG	2037

QY	1844	GAGTTTCCAGAGTAAAGCTGACACTGGGCAAGCCCTTGGAGAAAGGTGCTTTGGGCAA	1903
Db	2038	GAGTTTCCAGAGTAAAGCTGACACTGGGCAAGCCCTTGGAGAAAGGTGCTTTGGGCAA	2097
QY	1904	GTGGTCATGGCGAAGCAGTGGGAATTGACAAACAGCAAGCCCAAGAGAGCGGTCACCGTG	1963
Db	2098	GTGGTCATGGCGAAGCAGTGGGAATTGACAAACAGCAAGCCCAAGAGAGCGGTCACCGTG	2157
QY	1964	GCCGTGAAGATGTTGAAGAATGATGCCACAGAAAGAAGCTTTCTGATCTGGGTCCAGAG	2023
Db	2158	GCCGTGAAGATGTTGAAGAATGATGCCACAGAAAGAAGCTTTCTGATCTGGGTCCAGAG	2217
QY	2024	ATGGAGATGATGAAGATGATTTGGGAAACAAGAATATCATTAATCTTTGGAGCCCTGC	2083
Db	2218	ATGGAGATGATGAAGATGATTTGGGAAACAAGAATATCATTAATCTTTGGAGCCCTGC	2277
QY	2084	ACACAGATGGGCGCTCTATGTATGATAGTATGCTCTTAAGGCAACCTCCGAGAA	2143
Db	2278	ACACAGATGGGCGCTCTATGTATGATAGTATGCTCTTAAGGCAACCTCCGAGAA	2337
QY	2144	TACCTCCGAGCCCGGAGGCCACCCGGGATGGAGATCTCTATGACATTAAACGGTTCCT	2203
Db	2338	TACCTCCGAGCCCGGAGGCCACCCGGGATGGAGATCTCTATGACATTAAACGGTTCCT	2397
QY	2204	GAGGAGCAGATGACCTTCAGAGAAGCTTGGTGTATGACCTTAACAGCTGGCCAGACGATG	2263
Db	2398	GAGGAGCAGATGACCTTCAGAGAAGCTTGGTGTATGACCTTAACAGCTGGCCAGACGATG	2457
QY	2284	GAGTACTTGGCTTCCCAAAAATGTATTATCATGAGATTGAAGGACAGAAATGTTTTGGTA	2323
Db	2458	GAGTACTTGGCTTCCCAAAAATGTATTATCATGAGATTGAAGGACAGAAATGTTTTGGTA	2517
QY	2324	ACAGAAAACAATGTGTATGAAAAATAGCAGACTTTGGACTCGCCAGAGATATCAACAATTA	2383
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QY	2384	GACTATTACAAAAGACCAACCAATGGGGGCTTCCAGTCAAGTGGATGGCTCCAGAAACC	2443
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QY	2444	CTGTTGTAGATGATACACTCATCAGAGTATGTCTGTGCTTCGAGGTGTTAATGTGG	2503
Db	2638	CTGTTGTAGATGATACACTCATCAGAGTATGTCTGTGCTTCGAGGTGTTAATGTGG	2697
QY	2504	GAGATCTTCACTTTAGGGGGCTCGCCCTAACCCAGGGAATCCCGTGGAGAACTTTTAAAG	2566
Db	2698	GAGATCTTCACTTTAGGGGGCTCGCCCTAACCCAGGGAATCCCGTGGAGAACTTTTAAAG	2752
QY	2564	CTGCTGAAGGAAGGACACAGAAATGATTAAGCAGCAACCTGACCAAGAACTGTACATG	2623
Db	2758	CTGCTGAAGGAAGGACACAGAAATGATTAAGCAGCAACCTGACCAAGAACTGTACATG	2811
QY	2624	ATGATGAAGGACCTGTTGGCATGCACTGCCCTCCAGAGACCAAGCTTCAAGCAGTTGCTTA	2688
Db	2818	ATGATGAAGGACCTGTTGGCATGCACTGCCCTCCAGAGACCAAGCTTCAAGCAGTTGCTTA	2877
QY	2684	GAAGACTTGGATCGAATTTCTCACTTCCACAAACCAATGAG	2722
Db	2878	GAAGACTTGGATCGAATTTCTCACTTCCACAAACCAATGAG	2916

Search completed: October 2, 2006, 18:47:12
Job time : 1108 secs

GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: October 2, 2006, 17:04:22 ; Search time 14063 Seconds
(without alignments)
12350.526 Million cell updates/sec

Title: US-10-701-263-1

Perfect score: 3106

Sequence: 1 cccgcgagcaagttgtgtg.....ttctcgagcagtgacgcgc 3106

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

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12: gb_est13:*
13: gb_est14:*
14: gb_est15:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2305.4	74.2	2460	14	DO037912 Homo sapi
2	2166	69.7	3523	6	BC096749 Homo sapi
3	1384.4	44.6	2817	6	CR857280 Pongo pyg
4	1177.2	37.9	2295	14	DO037913
5	1086.4	35.0	3513	6	CR859698 Pongo pyg
6	1050.2	33.8	4050	6	AK049704 Mus muscu
7	1001.4	32.2	3259	6	AK028354 Mus muscu
8	906.6	29.2	4150	6	AK143582 Mus muscu
9	905.4	29.2	3761	6	AK163495 Mus muscu
10	777.4	25.0	885	3	BQ438964 AGENCOURT
11	759.6	24.5	898	1	DN102332 AGENCOURT
12	755.6	24.3	898	1	DN102332 AGENCOURT
13	735	23.7	757	5	CD643272 AGENCOURT
14	728	23.4	3146	6	AK084850 Mus muscu
15	719	23.1	2218	6	AK081810 Mus muscu
16	705.2	22.7	818	10	CB217005 NTSC_nq11
17	704.4	22.7	722	9	DF608827 LB0161.CR
18	700.4	22.5	924	2	BI659907 603302485

20	697.2	22.4	834	2	BG698600 602658361
21	693.6	22.3	3133	6	AK085723 Mus muscu
22	693.4	22.3	1013	2	BI656483 603285918
23	692.8	22.3	905	2	BI655023 603283291
24	692.4	22.3	791	2	BI656640 603284992
25	692	22.3	692	2	BI656640 603284992
26	690	22.3	726	8	CN345543 AGENCOURT
27	687.6	22.1	909	2	CN345543 170005998
28	685.8	22.1	909	2	BI661393 603304679
29	684.8	22.0	946	2	DN822797 UMC-Demil
30	682.4	22.0	929	2	BI558570 603240571
31	677.2	21.8	693	3	DR002343 TC112366
32	676.8	21.8	680	5	BM792391 K-EST0072
33	672.2	21.6	720	2	CD675167 Es19g10.Y
34	671.6	21.6	879	2	DR001520 TC124541
35	664.8	21.4	797	4	BI654011 603380903
36	664.2	21.4	836	2	CA318181 UI-M-FW-
37	661.4	21.3	836	2	BI853502 603381107
38	660.4	21.3	787	2	BI853502 603240792
39	660.4	21.3	774	2	BI661662 603305601
40	660.4	21.3	826	2	BI660473 603303440
41	660	21.2	852	2	BI658887 603301446
42	659.8	21.2	808	2	BI653362 603379944
43	658.4	21.2	771	8	BI684439 602798521
44	658.4	21.2	910	2	CR629587 DKFZP469H
45	657.8	21.2	965	2	BI659067 603301716

ALIGNMENTS

RESULT 1
LOCUS DO037912
DEFINITION Homo sapiens FGFR2 gene, VIRTUAL TRANSCRIPT, partial sequence.
ACCESSION DO037912
VERSION DO037912.1 GI:66889121
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae; Homo
REFERENCE 1 (bases 1 to 2460)
Nielsen,R., Bustamante,C., Clark,A.G., Gianowski,S., Sackton,T.B., Hubisz,M.J., Pedel-Alon,A., Tanenbaum,D.M., Civejlo,D., White,T.J., Srinisky,J.J., Adams,M.D. and Cargill,M.
A Scan for Positively Selected Genes in the Genomes of Humans and Chimpanzees
(et) Plos Biol. 3 (6), E170 (2005)
JOURNAL PLoS Biol. 3 (6), E170 (2005)
AUTHORS 15869325
TITLE 2 (bases 1 to 2460)
Nielsen,R., Bustamante,C., Clark,A.G., Gianowski,S., Sackton,T.B., Hubisz,M.J., Pedel-Alon,A., Tanenbaum,D.M., Civejlo,D., White,T.J., Srinisky,J.J., Adams,M.D. and Cargill,M.
DIRECT SUBMISSION
Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment. Translation starts at the beginning of alignment.
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location/Qualifiers
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/locus_tag="HC7772"
ORIGIN

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Matches 2393; Conservative	0;	Mismatches 61;	Indels 21;	Gaps 3;

QY	413	ATGTGACGTGGGGTGGTTTCATCTGGCTGGTGGTCAACATGGCAACTGTTGGCTGG	478
Db	1	ATGGTCAAGCTGGGGGTCTGTTTCATCTGGCTGGTGGTCAACATGGCAACTGTTGGCTGG	60
QY	479	GCCCGGCGCTCTCTCAGTTTATGTGAGATPACACATTAAGGCCAGAAAGCCACCAACC	538
Db	61	GCCCGGCGCTCTCTCAGTTTATGTGAGATPACACATTAAGGCCAGAAAGCCACCAACC	120
QY	539	AAATPACCAATCTCTCAACCAAGGTGACGTGGCTGGCCAGGGGAGTGGCTPAGAGGTG	598
Db	121	AAATPACCAATCTCTCAACCAAGGTGACGTGGCTGGCCAGGGGAGTGGCTPAGAGGTG	180
QY	599	CGCTGGCTGTGAAGAAGATGCGCGCGTGATCAGTTTGGACTPAAAGATGGGGGTGCACTTGGGG	658
Db	181	CGCTGGCTGTGAAGAAGATGCGCGCGTGATCAGTTTGGACTPAAAGATGGGGGTGCACTTGGGG	240
QY	659	CCCAACCAATPAGACAGTCTTATTTGGGGAGTACTTTCAGATPAAAGGCGCCACACTPAGA	718
Db	241	CCCAACCAATPAGACAGTCTTATTTGGGGAGTACTTTCAGATPAAAGGCGCCACACTPAGA	300
QY	719	GACTTCGGGCTCTATGCTTATGCTTATACGTGACGTGAGACTGTAAACATGGTAATTC	778
Db	301	GACTTCGGGCTCTATGCTTATGCTTATACGTGACGTGAGACTGTAAACATGGTAATTC	360
QY	779	ATGTGATATGTCAACGATGCCATCTCATCCGGAATGATGAGATGACACCGATGTGCG	838
Db	361	ATGTGATATGTCAACGATGCCATCTCATCCGGAATGATGAGATGACACCGATGTGCG	420
QY	839	GAAGATTTTGTCAGTGAGACAATPACAACAAGAGACACATCTGAGCCACACAGAA	898
Db	421	GAAGATTTTGTCAGTGAGACAATPACAACAAGAGACACATCTGAGCCACACAGAA	480
QY	899	AAAGATGGAAGGCGGCTCATGCTGTGGCTGGCGCAACACTGTCAAGTTTGGCTGGCCA	958
Db	481	AAAGATGGAAGGCGGCTCATGCTGTGGCTGGCGCAACACTGTCAAGTTTGGCTGGCCA	540
QY	959	GCCGGGGGGAACCCCAATGCCAACCAATGCGGTGGCTGAAAACCGGGAAGAGATTTAAGCAG	1018
Db	541	GCCGGGGGGAACCCCAATGCCAACCAATGCGGTGGCTGAAAACCGGGAAGAGATTTAAGCAG	600
QY	1019	GAGCATGCGATTTGAGAGGCTACAAGGTAAGAAACCAAGCATGAGAACCTTATATGGAAGT	1078
Db	601	GAGCATGCGATTTGAGAGGCTACAAGGTAAGAAACCAAGCATGAGAACCTTATATGGAAGT	660
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QY	1199	GGAATGCGCGGAAAGGCTCCACAGTGTGTGGAGAGACGTATGATTTGTCTGAAGGTT	1258
Db	781	GGAATGCGCGGAAAGGCTCCACAGTGTGTGGAGAGACGTATGATTTGTCTGAAGGTT	840
QY	1259	TACAGTGTATGCCACAGCCCACTCATCATGTGATCAAGCACGTGTGAAAAGAACCGCAGTAAA	1318
Db	841	TACAGTGTATGCCACAGCCCACTCATCATGTGATCAAGCACGTGTGAAAAGAACCGCAGTAAA	900
QY	1319	TACGGGCCCCGACGGGCTGGCCTCACTCAAGGTTCTCAAGCACTGGGGATPAAATATGTTCC	1378
Db	901	TACGGGCCCCGACGGGCTGGCCTCACTCAAGGTTCTCAAGGCTGGGGATPAAACACAG	960
QY	1379	AATGACAGAAGTCTGGCTGTG-----TCAATGTGACGAGGCGGAGTCTGGGGAATAT	1432
Db	961	GACAAAGAGATGAGGTTCTCTATATTTGGAAATGTATCTTTTGAAGACGCTGGGGAAATAT	1020
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Db	1021	ACGCTTGGCGGGTAATTCATATGGGATATTCCTTTCACTCTGATGAGTTGACAGTTCTG	1080
Qy	1493	CCAAAACAGACAGCGCTCGAAGAGAAAGAGATTCACGCTTCCCGACATACCTGGAG	1552
Db	1081	CC-----AGGCGCTGGAGAGAGAAAGAGATTACAGCTTCCCGACATACCTGGAG	1131
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Db	1132	ATATCCATTTTACTGCATAGGGGGTCTTCTTAATGCGCTGTATGCTGTAAAGTCATCTG	1191
Qy	1613	TGCGGAATGAAGAACAGACCAAGAACCGACCTTCACGACCCGCGCTGTCACAAG	1672
Db	1192	TGCGGAATGAAGAACAGACCAAGAACCGACCTTCACGACCCGCGCTGTCACAAG	1251
Qy	1673	CTGACCAAAAGTATCCCCCTGCGGAGACAGGTAAACGTTTCGCGTGAATCAGCTCTCC	1732
Db	1252	CTGACCAAAAGTATCCCCCTGCGGAGACAG-----GTTTCGCGTGAATCAGCTCTCC	1305
Qy	1733	ATGAATCTCCAACACCCCGCTGTGTAGGATTAACAACGCGCTCTTTCACAAGGACAGACC	1792
Db	1306	ATGAATCTCCAACACCCCGCTGTGTAGGATTAACAACGCGCTCTTTCACAAGGACAGACC	1365
Qy	1793	CCCAATGCTGCGAGGGGTCTCCGAGTATGAATTCACAAGAACCCAAATATGGAGTTTCCA	1852
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Qy	1853	AGAAATTAAGTCGACACTGGGAGAACCCCTGGGAGAAAGTTGCTTTGGGCAAGTGTATG	1912
Db	1426	AGAAATTAAGTCGACACTGGGAGAACCCCTGGGAGAAAGTTGCTTTGGGCAAGTGTATG	1485
Qy	1913	GCGAGACGATGGGGAATTGACAAAGACAGGCCCAAGAGGGCGGTCAACGTGGCGGTGAAG	1972
Db	1486	GCGAGACGATGGGGAATTGACAAAGACAGGCCCAAGAGGGCGGTCAACGTGGCGGTGAAG	1545
Qy	1973	ATGTTGAAGAATGATGCCACAGAGAAAGACCTTCTGTATCTGTGTACAGATGGAATG	2032
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Qy	2153	GCCCGAGAGCCACCCGGGATGGAATCTCTATGACATTTAACGTGTCTCTGAGAGAGAG	2212
Db	1726	GCCCGAGAGCCACCCGGGATGGAATCTCTATGACATTTAACGTGTCTCTGAGAGAGAG	1785
Qy	2213	ATGACCTTCAAGAGCTTGGTGTCAATGACCTAACAGCGTGGCGAGCGGATGGAATCTG	2272
Db	1786	ATGACCTTCAAGAGCTTGGTGTCAATGACCTAACAGCGTGGCGAGCGGATGGAATCTG	1845
Qy	2273	GCTTCCCAAAATATGATTCATCGAGATTATAGCAGCCAGAAATGTTTGGTAAACAGAAAC	2332
Db	1846	GCTTCCCAAAATATGATTCATCGAGATTATAGCAGCCAGAAATGTTTGGTAAACAGAAAC	1905
Qy	2333	AATGTGATGAATAATGACAGCTTTGGACTGCGCAGAGATATTCACAATATATGACTATTAAC	2392
Db	1906	AATGTGATGAATAATGACAGCTTTGGACTGCGCAGAGATATTCACAATATATGACTATTAAC	1966
Qy	2393	AAAAAGACCAACATGCGCGGCTTCCATTCACAAGTGAAGGCTCCAGAGACCCCTGTTTAT	2455
Db	1966	AAAAAGACCAACATGCGCGGCTTCCATTCACAAGTGAAGGCTCCAGAGACCCCTGTTTAT	2025
Qy	2453	AGAGATTAACATCATCAGATGATGTCTGTGCTCTTGGGGGTGTTAATGTGGAGATCTTC	2512
Db	2026	AGAGATTAACATCATCAGATGATGTCTGTGCTCTTGGGGGTGTTAATGTGGAGATCTTC	2089
Qy	2513	ACTTTAGGGGGCTGCGCCTTACCCAGAGATTCCTGAGAGAACTTTTAACTGTGTAAG	2572

Db	2086	ACTTTAAGGAGGCTGGCCCTTACCAGGAGATTCGCCGGAGGAACTTTTAAAGCTCTGAAG	2145
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Db	2146	GAAGGACACAGAAATGAGATTAAGCCAGCCCACTGACACAAAGAACTGTACATATGATGAAG	2205
QY	2633	GACGTGGGCAATGACATGAGCCCTCCAGAGACCAACAGTTCAAGGATGGTGAAGACCTGG	2692
Db	2206	GACGTGGGCAATGACATGAGCCCTCCAGAGACCAACAGTTCAAGGATGGTGAAGACCTGG	2265
QY	2693	GATCGAAATTCCTCACTCTGACAAACCAATGAGAAATTAATGACCTCAGCCAACTCTCGAA	2752
Db	2266	GATCGAAATTCCTCACTCTGACAAACCAATGAGAAATTAATGACCTCAGCCAACTCTCGAA	2325
QY	2753	CAGTAATTCACCTAGTTACCTCTGACACAAAGAACTTGTCTTCTTCAAGAGATGATTCGTT	2812
Db	2326	CAGTAATTCACCTAGTTACCTCTGACACAAAGAACTTGTCTTCTTCAAGAGATGATTCGTT	2385
QY	2813	TTTTCCTCAGAGCCCAATGAGCAACCAAGCTCTCTCTGATGATTCACATATAAGGCGC	2872
Db	2386	TTTTCCTCAGAGCCCAATGAGCAACCAAGCTCTCTCTGATGATTCACATATAAGGCGC	2445
QY	2873	AGTGTAAAAACATGA 2887	
Db	2446	AGTGTAAAAACATGA 2460	
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VERSION	BC096749.1	GI:66911819	
KEYWORDS	HTC.		
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ORGANISM	Homo sapiens		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.		
REFERENCE	1 (bases 1 to 3523)		
AUTHORS	Strausberg,R.L., Feingold,R.A., Grouse,L.H., Derge,J.G., Klausner,R.D., Collins,F.S., Wagner,L., Shemen,C.M., Schuler,G.D., Altschul,S.F., Zeeberg,B., Buatow,K.H., Schaefer,C.F., Bat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F., Ditchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Stepleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L., Scheetz,T.E., Brownstein,M.J., Uedin,T.B., Toshitsuki,S., Carninci,P., Prange,C., Rana,S.S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mullahy,S.J., Bosak,S.A., McMan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W., Villalón,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahey,J., Helton,E., Kettelman,M., Madan,A., Rodriguez,S., Sanchir,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y., Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Butlerfield,Y.S., Krzywiński,M.I., Skalka,U., Smalhus,D.E., Scherch,A., Schein,J.E., Jones,S.J. and Marra,M.A.		
CONSRMT	Mammalian Gene Collection Program Team		
TITLE	Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences		
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)		
PUBMED	12477932		
REFERENCE	2 (bases 1 to 3523)		
AUTHORS	NIH MGC Project		
CONSRMT	Direct Submission		
TITLE	Submitted (01-JUN-2005) National Institutes of Health, Mammalian Gene Collection (MGC), Bethesda, MD 20892-2590, USA		
JOURNAL	NIH-MGC Project URL: http://mgc.nci.nih.gov		
REMARK	Contact: MGC help desk		
COMMENT	Email: cgaeph-r@mail.nih.gov		

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 SOURCE Pongo pygmaeus (orangutan)
 ORGANISM Pongo pygmaeus
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 REFERENCE 1 (bases 1 to 2817)
 AUTHORS Bahr, A., Lauber, J., Mewes, H. W., Weil, B., Amid, C., Oesanger, A., Fobo, G., Han, M., and Wiemann, S.
 CONSRTM The German cDNA Consortium
 TITLE Direct Submission
 JOURNAL Submitted (12-NOV-2004) MIPS, Ingolstaedter Landstr. 1, D-85764 Neuberg, GERMANY
 COMMENT
 Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ), Email: s.wiemann@dkfz-heidelberg.de; sequenced by Qiagen (Hilden/Germany) within the cDNA sequencing consortium of the German Genome Project.
 This clone (DKFZp469H1521) is available at the RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH in Berlin, Germany.
 Please contact RZPD for ordering:
 http://www.rzpd.de/cgi-bin/products/c1.cgi?cloneID=DKFZp469H1521
 Further information about the clone and the sequencing project is available at http://mips.gsf.de/projects/cdna/.
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FEATURES

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TITLE		Direct Submission	
JOURNAL		Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA	
COMMENT		This sequence was made by sequencing genomic exons and ordering them based on alignment. Translation starts at the beginning of alignment.	
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RESULT 5
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LOCUS      CR859698      3513 bp      mRNA      linear      HTC 12-NOV-2004
DEFINITION Pongo pygmaeus mRNA; cDNA DKFp469L2025 (from clone DKFp469L2025).
ACCESSION CR859698
VERSION    CR859698.1 GI:55730268
KEYWORDS   HTC.
SOURCE     Pongo pygmaeus (orangutan)
ORGANISM   Pongo pygmaeus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Homiidae; Pongo.
REFERENCE  1 (bases 1 to 3513)
            Wambute,R., Heubner,D., Mewes,H.W., Weil,B., Amlid,C., Osanger,A.,
            Fobo,G., Han,M. and Wiemann,S.
            The German cDNA Consortium
            Direct Submission
            Submitted (12-NOV-2004) MIPS, Ingolstaedter Landstr.1, D-85764
            Neuberberg, GERMANY
            Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
            Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
            sequenced by Agowa (Berlin/Germany) within the cDNA sequencing
            consortium of the German Genome Project.
            This clone (DKFp469L2025) is available at the RZPD Deutsches
            Ressourcenzentrum fuer Genomforschung GmbH in Berlin, Germany.
            Please contact RZPD for ordering:
            http://www.rzpd.de/cgi-bin/products/cl.cgi?cloneID=DKFp469L2025
            Further information about the clone and the sequencing project is
            available at http://mips.gsf.de/projects/cdna/.
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ORIGIN

Query Match 35.0%; Score 1086.4; DB 6; Length 3513;
 Best Local Similarity 68.8%; Pred. No. 3.2e-307;
 Matches 1578; Conservative 0; Mismatches 681; Indels 33; Gaps 5;

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 Db 832 GATCAACACACAGTACAGCTGATGTGTGAGAGGATCCCTCAACCGACCATCTTCG 891
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 Db 1957 ATCTGCGCTTCAAGAGTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2016
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 Db 2017 AGGACATGTGATGAATGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2076

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RESULT 6
AK049704
LOCUS
DEFINITION
AK049704 4050 bp mRNA linear HTC 02-SEP-2005
Mus musculus 12 days embryo spinal cord cDNA, RIKEN full-length
enriched library, clone: C530043G19 product: fibroblast growth factor
receptor 1, full insert sequence.

ACCESSION
AK049704
VERSION
AK049704.1 GI:26093593
KEYWORDS
HTC; CAP trapper.
SOURCE
Mus musculus (house mouse)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus.

REFERENCE
AUTHORS
Carninci, P. and Hayashizaki, Y.
TITLE
High-efficiency full-length cDNA cloning
JOURNAL
Meth. Enzymol. 303, 19-44 (1999)
PUBMED
10349636
REFERENCE
AUTHORS
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Komano, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
TITLE
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL
Genome Res. 10 (10), 1617-1630 (2000)
PUBMED
11042159
REFERENCE
AUTHORS
Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,
Komano, H., Akiyama, J., Nishi, K., Kitsuai, T., Tashiro, H., Itoh, M.,
Sumi, N., Ishii, Y., Nakamura, S., Harada, M., Nishine, T., Harada, A.,
Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
Fujisawa, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Wataniki, M.,
Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J.,
Okazaki, Y., Muramatsu, M., Inoue, Y., Kita, A. and Hayashizaki, Y.
TITLE
RIKEN integrated sequence analysis (RISA) system-384-format

sequencing pipeline with 384 multicapillary sequencer
Genome Res. 10 (11), 1757-1771 (2000)
11076861

4
The RIKEN Genome Exploration Research Group Phase II Team and the
PANTOM Consortium.
Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)

5
The PANTOM Consortium, the RIKEN Genome Exploration Research Group
Phase I and II Team.
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)

6
RIKEN Genome Exploration Research Group, Genome Science Group
(Genome Network Core Team) and the PANTOM Consortium.
Antisense Transcription in the Mammalian Transcriptome
Science 309, 1564-1566 (2005)

7
The PANTOM Consortium, Riken Genome Exploration Research Group and
Genome Science Group (Genome Network Project Core Group).
The Transcriptional Landscape of the Mammalian Genome
Science 309, 1559-1563 (2005)

8 (bases 1 to 4050)
Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,
Fukuda, S., Furuno, M., Hanigaki, T., Hara, A., Hashizume, W.,
Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T.,
Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T.,
Kato, H., Kawai, J., Kojima, Y., Kondo, S., Komano, H., Kouda, M.,
Koya, S., Kuribara, C., Matsuyama, T., Miyazaki, A., Murata, M.,
Nakamura, M., Nishi, K., Nomura, K., Nunazaki, R., Ohno, M., Ohsato, N.,
Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N.,
Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T.,
Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S.,
Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,
Muramatsu, M. and Hayashizaki, Y.
Direct Submission

TITLE
JOURNAL
Submitted (16-JUN-2001) Yoshinide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
Kanagawa, 230-0045, Japan (E-mail: genome-res@gscc.riken.jp.
URL: http://genome-gsc.riken.jp/, Tel: 81-45-503-9222,
Fax: 81-45-503-9216)

COMMENT
cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Please visit our web site for further details.
URL: http://genome-gsc.riken.jp/
URL: http://fantom.gsc.riken.jp/
URL: http://location.qualifiers

FEATURES
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ORIGIN
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Best Local Similarity 68.2%; Pred. No. 1.5e-296;
Matches 1577; Conservative 0; Mismatches 698; Indels 38; Gaps 7;

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OY	626	-ATCAGTTGACCTAAGGATGGGGGTGCACCTTGGGGCCCAACAATATGACAGTGTATTAG	684
Db	916	CATCAACTGGCTGGGGATGGGGTGTGAGCTGTGTGAAGCAACCGTACCCGATCAACAG	975
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Db	1036	CAGCAGCCCTCTGTGACAGCATTAACCACTTACTTCGGTCAATGTCTCAATGACACTCC	1095
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QY	2290	TCATCGAATTTTACGAGCCAGAAATGTTTGTGTAAACAGAAAACAATGTATGAATATAGC	2349
Db	2579	ACAACGGAACCTGTGCTGATGAAGCTCTGTGTGACCGAGATATACGTATATGAAGATGCG	2638
QY	2350	AGACTTTGACTCGCCAGAGATATCAACAATATATGATCTATTAACAAAAAGACCAACATAG	2409
Db	2639	AGACTTTGGCTTATGCTCGAGACATTCATCAATATGATCTATTAACAAAAACCAACCAAGG	2698
QY	2410	GGGGTTTCAATGACAGTGTGATGGGCTCCAGAAAGCCGTGTTATATGATATCACTCATCA	2469
Db	2699	CCAGGTGCTGTGAAGTGAATGCCCCCTGAGGCGTTGTTTACCGGATCTTACACACACA	2758
QY	2470	GAGTATGTCTGTGCTCTTCGAGGTGTATATGTGGAGATCTTCACTTTAGGGGCTGCGC	2529
Db	2759	GAGCATATGTGTCTTTTGGAGTGCTCTGTGGAGATCTTCACTCGGGTGCTGCC	2818
QY	2530	CTACCCAGAGATTCCTCGTAGAGAACTTTTATAGCTGCTGAAGAGAGACACAGAAATGA	2589
Db	2819	ATATCCCCGGTGTGCTGTGAGAGAACTTTTCAAGCTGTCTGAAGAGAGGTATCATATGATGA	2878
QY	2590	TAAAGCAGCCAACTTCCAAACGAATGTATCAATGATATGATGAGGGAGCTGTGGATGACAGT	2649
Db	2879	CAAAGCCAGTAACTGTACCAATGAAGCTGTACATGATGATGAGGGAGCTGTGGATGACAGT	2938
QY	2650	GGCCTTCCAGAGACCAAGTTCAACAGTGTGTATAGACATTTGATTCGAAATTTCTCATCT	2709
Db	2939	GGCCTTCTAGAGACTTACCTTACACAGATGTGTGAGAGACCTGAGCCGATGTGTGGCTT	2998
QY	2710	CAACAACCAATGAGAAATCTTGAACCTTACGCCAACCTCTCGAACATTTACCTTATGTTA	2769

Db	Accession	Source	Organism	Version	Keywords	Definition	LOCUS	Result 7
Db	2999	GACCTCCACCAAGAGATTTCTGAGCTTCCATACCGCTGACCAAGTACTACCCAGCTT	3058					
Qy	2770	CCCTGACACAGAAAGTT---CTTGTCTTCAGAGATGATTTCTGTTTTTTCAGACCC	2826					
Db	3059	TCCGAGACACAGGAGCTCCACCTGTCTCTGACGGGAGAGACTGTGCTCTCTCATGAGCC	3118					
Qy	2827	CATGCTTACGACACCATGCTTCTCTCAGTATCC	2859					
Db	3119	GTTACTGAGAGAGCCCTGTCTGCTTCAGACACC	3151					
REFERENCE	AK028354	3259 bp	mRNA	linear	HTC 02-SEP-2005			
LOCUS	AK028354							
DEFINITION	AK028354	18 days pregnant adult female placenta and extra embryonic tissue cDNA, RIKEN full-length enriched library, clone:3830408H21 product:fibroblast growth factor receptor 1, full insert sequence.						
ACCESSION	AK028354							
VERSION	AK028354.1	GI:26390449						
KEYWORDS	HTC; CAP trapper.							
SOURCE	Mus musculus (house mouse)							
ORGANISM	Mus musculus							
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.							
AUTHORS	Carninci, P. and Hayashizaki, Y.							
TITLE	High-efficiency full-length cDNA cloning							
JOURNAL	Meth. Enzymol. 303, 19-44 (1999)							
PUBMED	10349636							
AUTHORS	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y.							
TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes							
JOURNAL	Genome Res. 10 (10), 1617-1630 (2000)							
PUBMED	11042159							
AUTHORS	Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Kono, H., Akiyama, J., Nishi, K., Kitsuana, T., Tashiro, H., Itoh, M., Sun, N., Ishii, Y., Nakamura, S., Hazada, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kaishwagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watanabe, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A., and Hayashizaki, Y.							
TITLE	RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer							
JOURNAL	Genome Res. 10 (11), 1757-1771 (2000)							
PUBMED	11076861							
AUTHORS	The RIKEN Genome Exploration Research Group Phase II Team and the PANTOM Consortium.							
TITLE	Functional annotation of a full-length mouse cDNA collection							
JOURNAL	Nature 409, 685-690 (2001)							
PUBMED	1176861							
AUTHORS	The PANTOM Consortium, the RIKEN Genome Exploration Research Group Phase I and II Team.							
TITLE	Analysis of the mouse transcriptome based on functional annotation							
JOURNAL	Nature 420, 563-573 (2002)							
PUBMED	12420							
AUTHORS	RIKEN Genome Exploration Research Group, Genome Science Group (Genome Network Core Team) and the PANTOM Consortium.							
TITLE	Antisense Transcription in the Mammalian Transcriptome							
JOURNAL	Science 309, 1564-1566 (2005)							
PUBMED	16124							
AUTHORS	The FANTOM Consortium, Riken Genome Exploration Research Group and Genome Science Group (Genome Network Project Core Group).							
TITLE	The Transcriptional Landscape of the Mammalian Genome							
JOURNAL	Science 309, 1559-1563 (2005)							
PUBMED	16124							
AUTHORS	(bases 1 to 3259)							

DB	Query Match	Score	Length	3259;
874	AGCACATATCGGACCAACAGAAAGAGAAAGACGCGTCATCGTGTGCTCGGAGC	32.2%	70.4%	Pred. No. 3.3e-282;
385	AGCTCCCTATCGACATCCCAAGAGAAATGAGAGAAACTGATCGATCGCGCCGCTGC	0;	Mismatches 566;	Indels 24; Gaps 4;

QY 934 CAACACTGTCAAGTTTCCTGCTCCAGCCGGGGGGAACCCAAATGCCAATGCCGTGCT 993
 Db 445 CAAGACGGTGAAGTTCAAGTTGCCGTCCAGTGGGACACCCAACTCCGCTGGTT 504
 QY 994 GAAAAACGGGAAGAGTTTAAGCAGAGAGATGCGATTGGAGGCTTCAAGGTACGAAACA 1053
 Db 505 GAAAAATGGCAAGAGTTTAAGCTGACCAACGAATTGGAGGCTTCAAGGTGCTATGC 564
 QY 1054 GCACGTGAGCCCTCATTAATGAGAAAGTGTGCTCCATCTGACAAAGGAAATTAATCTGT 1113
 Db 565 CACTTGAGCATCATTAATGAGATTTCTGTGTGCTTCTGACAAAGGCACTACCTGCAT 624
 QY 1114 AGTGAAGATGAATAACGGGTCCATCATCAACGTACCACTGATGTGTGGAGCCATC 1173
 Db 625 CGTGAAGATGATGATGAGGAGCATCAACACACTACAGCTTGAAGTGGAGAGATC 684
 QY 1174 GCCTTACCGGCCCCTATCTTCAAGCCGGAGTCCGGCAATGCTTCCACAGTGTGGAG 1233
 Db 685 TCCGCAACCGACCCATCTTCAAGGAGGCTGCTGCTCCAAAGAGAGTGGCCCTGGCAG 744
 QY 1234 AGACGTAGAGTTGTCTGCAAGTTTACAGTATGCGGACCCCACTCCAGTGAATCA 1293
 Db 745 CAATGTGAAGTTCAATGTGAATGATGATGATGATGATGATGATGATGATGATGATG 804
 QY 1294 GCACGTGAAAAAAGACGGAGTAAATACGGGCTCCAGCGGCTGCTTCAAGTGTCT 1353
 Db 805 GCACATTCAGAGTGAACGGGAGTAAATGATGCGGCAAGCAACTGCGTATGTCCAGATCT 864
 QY 1354 CAAGCACTGGGGATTAATAGTTCCATGCAAGAA-----GTGCTGCTGTGTGAAT 1407
 Db 865 GAAAGCTGTGAATTAATCAACCGAAGAGAAATGAGGTCTTCACTTACGAAATGT 924
 QY 1408 GACCGAGCGAGTGTGCGGGAATATATATATATATATATATATATATATATATATAT 1467
 Db 925 CTCTTTTGAAGATGCGGGGAGATATACGTGCTTGGGGTAACTCATGAGCTCTCCA 984
 QY 1468 CCAAGTCTGCTGCTCACTGCTCTGCAAAAGCAAGCGCTGGAAGAGAAAGAGAT 1527
 Db 985 TCACCTGATGTTGACCGTCT-----GGAAAGCTGGAAGAGACCAAGCTGT 1035
 QY 1528 TACAGTTTCCAGACTACCTGAGATACCATTTATCTGATAGAGGTCTTCTTAATGC 1587
 Db 1036 GATGACTTACCGCTTACCTGAGATCATTTATCTACCTACCGGGGCTTCTTATCTC 1095
 QY 1588 CTGTATGTGTAAACAGTATCTGTGCGGAATGAAGAACAGAGCAAGACCAAGCTT 1647
 Db 1096 CTGCAATGTTGGGCTGTGTATCATCTAATAAGTGAAGAGCGGACCAAGAGAGGACTT 1155
 QY 1648 CAGCAGCCAGCCGGCTGTGCAAGCTGAACAAACGTATCCCTGCGGAGACAGTTAC 1707
 Db 1156 CCATAGCCAGATGGCTGTGCAAGCTGGCCAAAGACATCCCTCTGCGGACAGGTATAC 1215
 QY 1708 AATTTCGCTGAGTCCAGCTCCCTCAATGAATCCAAACCCGCTGGTGAAGTAAACAC 1767
 Db 1216 AGTGTAGCTGACTTCAAGTCAATCAATGAATCTTGGGGTTCCTGCTGTGCGCCCTCAG 1275
 QY 1768 ACGCTCTCTTCAACGGCAGACACCCCAATGCTGAGAGGGGTCTCCAGATGAATTC 1827
 Db 1276 GCTC-----TCTTCAAGGGGAGCCCAATGCTGCTGAGGTCTCGAATATAGAGTCC 1329
 QY 1828 AAGAGACCCAAAAATGGAAGTTTCAAGAGATTAAGCTGAACCTGGGCAAGCCCTGGAGA 1887
 Db 1330 TAGAGATCCCGCTGGAGAGCTGCAAGAGACAGACTGTCTTATGGCAAACTTGGCGCA 1389
 QY 1888 AGGTTCCTTTGGCAGTGTGATGCGGAGAGAGTGGGAATTTGAAGAGACAAAGCCAA 1947
 Db 1390 GGGCTGCTTCCGGCAGGTGTGTGTGCTGAGGCAATCGGCTGGATTAAGAGCAAAACCA 1449
 QY 1948 GAGAGCGGTCAACGTGCGGTGAAGATTTGAAGATGATGCAAGAGAAAGACCTTTC 2007
 Db 1450 CCGTGTGACCAAGTGGCCGTGAAGATTTGTAAGTCCAGACGCAACGAGAGAGACCTGTC 1509

QY 2008 TGATCTGTGTGAGAGATGAGATGAATGAATGATTTGGGAAACAGAATATATATAA 2067
 Db 1510 GGAATCTATCTGAGAGATGAGATGAATGAATGATTTGGAGAGCAAGATATATATCA 1569
 QY 2068 TCTTCTTGGAGCTGCAACAGATGGGCTCTCTATGTACATAGTGAATGCTCTTAA 2127
 Db 1570 CTTTCTTGGAGCTGCAACAGATGATGCTCTTATGTATGATGATGAGTACGCTTCAA 1629
 QY 2128 AGGCAACCTCCAGAAATCTCCGAGCCCGGAGGCCACCCGGAGTGAAGTACTCTATGA 2187
 Db 1630 AGGCAATCTCCGGAGATATCTACAGGCCCGGAGGCTCTGGGCTGAGATCTCTATTA 1689
 QY 2188 CATTAACCGTGTCTGAGAGAGATGACCTTCAGAGACTTGTGTATGATCACTTACA 2247
 Db 1690 CCCAGCCCAACCCCGAGAGACGCTGTCTTCAAGAGTGTGATCTGTGCTATCA 1749
 QY 2248 GCTGCGCAGACGAGATGAGTACTTGGCTTCCAAAAATGATTTATGAGATTTAGAGC 2307
 Db 1750 GGTGGCTCGGGGAGATGAGTATCTTGGCTTAAAGAGTATACCGAGACTGGCTGC 1809
 QY 2308 CAGAAATGTTTGTATACAGAAAAAATGTGATGAATATAGACATTTGATCTGCCAG 2367
 Db 1810 TAGGAAGCTCTGTGTGACCGAGATTAAGTATGAATGACAGACTTGTGCTTAACTGC 1869
 QY 2368 AGATATCAACAAATPAGACTTATCAAAAAAGACCAACATGGGCGCTTCCAGTCAAGT 2427
 Db 1870 AGACATTCATATATTCAGACTTACAGAAAAACCAACAGCGGCTGCTGTGAAGTG 1929
 QY 2428 GATGCTTCCAGAACCCCTGTGTGATGATGATGATGATGATGATGATGATGATGATG 2487
 Db 1930 GATGGCCCTGAGGGGTGTTTGAACCGGATCTACACACACAGAGCAATGTGTGCTTT 1989
 QY 2488 CGGGGTGTTAATGTGAGATCTTCACTTTAGGGGGCTCGCCCTTACCAAGGATTCCT 2547
 Db 1990 TGAAGTCTCTTGTGGAGATCTTCACTGTGGGTGCTCCCATACCCGGTGTGCTGT 2049
 QY 2548 GAGGAACTTTTAAAGCTGTGAGAGAGAGAGACACAGATGATGATGATGATGATGATG 2607
 Db 2050 GAGGAACTTTTCAAGCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2109
 QY 2608 CAACGACTGTACATGATGATGAGAGAGCTGTGTGAGTCACTGCTCCAGAGACCAAC 2667
 Db 2110 CAATGAGCTGTACATGATGATGAGAGAGCTGTGAGTCACTGCTCCAGAGACTTAC 2169
 QY 2668 GTTCAAGAGTGTGATGAAGACTTGAATGAAATCTCACTGCAACCAATGAGGATA 2727
 Db 2170 GTTCAAGAGTGTGATGAAGACTTGAACCGGATGTGCTTGAACCTTCAACCAAGAGTA 2229
 QY 2728 CTGGAAGCTCAAGCCCACTTCGAAACAGTATTCACCTTGAATCCCTGAACAGAAATT- 2786
 Db 2230 TCTGAGCTGTTCATATCCGCTGAGACAGTATCTCAACCCAGCTTCCGACACAGAGCTC 2289
 QY 2787 --CTTGTCTTCAAGAGATGATGATGATGATGATGATGATGATGATGATGATG 2844
 Db 2290 CACGCTCTTCAAGGAGAGAGACTGTCTTCTCATGAGCGGTAACTGAGAGGCTCG 2349
 QY 2845 CTTTCTCAATATTC 2859
 Db 2350 TCTGCTCGACACC 2364

RESULT 8
 AKI43592 4150 bp mRNA linear HTC 21-SEP-2005
 LOCUS
 DEFINITION
 Mus musculus 6 days neonate spleen cDNA, RIKEN full-length enriched
 library, clone:FA2001106 product:fibroblast growth factor receptor
 3, full insert sequence.
 ACCESSION
 AKI43592.1 GI:74146955
 VERSION
 AKI43592.1
 KEYWORDS
 HTC; CAP trapper.
 SOURCE
 Mus musculus (house mouse)
 ORGANISM
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

- Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Murioidea; Muridae; Murinae; Mus.
- REFERENCE
AUTHORS
TITLE
JOURNAL
PUBMED
10349636
Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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AUTHORS
TITLE
JOURNAL
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11042159
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)
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11076861
Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Saeki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Katsunari, T., Tashiro, H., Itoh, M., Sumi, N., Iehi, Y., Nakamura, S., Hazama, M., Nishimura, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujitake, S., Inoue, K., Togawa, Y., Iizawa, M., Ohara, R., Mochizuki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kita, A., and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer
Genome Res. 10 (11), 1757-1771 (2000)
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Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y., Aizawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S., Arakawa, K., Iizawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamana, I., Saito, T., Okazaki, Y., Gojobori, T., Bono, H., Kasukawa, T., Saito, R., Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T., Fleischmann, W., Gaasterland, T., Gissi, C., King, B., Kochiwa, H., Kuehl, P., Lewis, S., Matsuo, Y., Nikaido, I., Pesole, G., Quackenbush, J., Schriml, L.M., Staudl, F., Suzuki, R., Tomita, M., Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H., Balderelli, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N., Carninci, P., de Bonaldo, M.F., Brownstein, M.J., Bult, C., Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D., Hofmann, M., Hume, D.A., Kamiya, M., Lee, N.H., Lyons, P., Marchionni, L., Mashima, J., Mazzarelli, J., Mombauts, P., Nordone, P., Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H., Sato, K., Schombach, C., Seya, T., Shibata, Y., Storch, K.F., Suzuki, H., Toyo-oka, K., Wang, K.H., Weitz, C., Whitaker, C., Wilming, L., Wynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawai, J., Kohsaki, S., and Hayashizaki, Y.
RIKEN Genome Exploration Research Group Phase II Team and the PANTOM Consortium
Functional annotation of a full-length mouse cDNA collection
Nature 409 (6821), 685-690 (2001)
- REFERENCE
AUTHORS
TITLE
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11217851
Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikaido, I., Oseato, N., Saito, R., Suzuki, H., Yamana, I., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schombach, C., Gojobori, T., Balderelli, R., Hill, D.P., Bult, C., Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H., Batalov, S., Beisel, K.W., Blake, J.A., Bradt, D., Brusic, V., Chochia, C., Corbani, L.E., Cousins, S., Dalla, R., Drganci, T.A., Fletcher, C.F., Forrest, A., Fraser, K.S., Gaasterland, T., Gariboldi, M., Gissi, C., Godik, A., Gough, J., Grimmond, S., Gustincich, S., Hirokawa, N., Jackson, I.J., Jarvis, E.D., Kanai, A., Kawai, J., Kawasawa, Y., Kedzierzki, R.M., King, B., Lyons, P.A., Maglott, D.R., Maltsev, L., Marchionni, L., McKenzie, L., Miki, H., Nagaishima, T., Numata, K., Okido, T., Pavan, W.J., Pertea, G., Pesole, G., Petrovsky, N., Pillai, R., Pavan, J.U., Qi, D., Ramachandran, S., Ravasi, T., Reed, J.C., Reed, P.J., Reid, J., Ring, B.Z., Ringwald, M., Sandoz, A., Schneider, C., Sempke, C.A., Seton, M., Shimada, K., Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale, R.D., Tomita, M., Verardo, R., Wagner, L., Wahlstedt, C., Wang, Y., Watanabe, Y., Wells, C., Wilming, L.G., Wynshaw-Boris, A., Yanagisawa, M., Yang, I., Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P., Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Arakawa, T., Fukuda, S., Shiraki, T., Waki, K., Kawai, J., Ishii, Y., Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Saeki, D., Shibata, K., Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S., Rogers, J., Birney, E., and Hayashizaki, Y.
CONSORTM
PANTOM Consortium
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420 (6915), 563-573 (2002)
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AUTHORS
TITLE
JOURNAL
PUBMED
12466851
Carninci, P., Kasukawa, T., Katayama, S., Gough, J., Frith, M.C., Maeda, N., Oyama, R., Ravasi, T., Lenhard, B., Wells, C., Kodzius, R., Shimokawa, K., Bajic, V.B., Brenner, S.E., Batalov, S., Forrest, A.R., Zavolan, M., Davis, M.J., Wilming, L.G., Aidinis, V., Allen, J.E., Ambesi-Impombato, A., Apweiler, R., Aurrelija, R.N., Bailey, T.L., Bansal, M., Baxter, L., Beisel, K.W., Bersano, T., Bono, H., Chalk, A.M., Chiu, K.P., Choudhary, V., Christoffels, A., Clutterbuck, D.R., Crowe, M.L., Dalla, E., Dalrymple, B.P., de Bono, B., Della Gatta, G., di Bernardo, P., Down, T., Engstrom, P., Fagiolini, M., Faulkner, G., Fletcher, C.F., Fukushima, T., Furuno, M., Futaki, S., Gariboldi, M., Georgii-Hemming, P., Gingeras, T.R., Gojobori, T., Green, R.E., Gustincich, S., Harbers, M., Hayashi, Y., Hensch, T.K., Hirokawa, N., Hill, D., Hummel, L., Iacono, M., Ikeo, K., Iwama, A., Ishikawa, T., Jakt, M., Kanapin, A., Katoh, M., Kawasawa, Y., Keisio, J., Kizumura, H., Kitano, H., Kohli, G., Krishnan, S.P., Kruger, A., Kummerfeld, S.K., Kurochkin, I.V., Lareau, L.F., Lazarevic, D., Lipovich, L., Liu, J., Liuni, S., McWilliam, S., Madan, B., Mader, M., Marchionni, L., Matsuda, H., Matsuzawa, S., Miki, H., Miyagishi, K., Miyake, S., Morris, K., Mottagui-Tabar, S., Mulder, N., Nakano, N., Nakachi, H., Ng, P., Nilsson, R., Nishiguchi, S., Nishikawa, S., Nori, P., Ohara, O., Okazaki, Y., Orlando, V., Pang, K.C., Pavan, W.J., Pavoni, G., Persole, G., Petrovsky, N., Piazza, S., Reed, J., Reid, J.F., Ring, B.Z., Ringwald, M., Rosi, B., Ruan, Y., Salzberg, S.L., Sandoz, A., Schneider, C., Schombach, C., Sekiguchi, K., Sempke, C.A., Seno, S., Sessa, L., Sheng, Y., Shibata, Y., Shimada, H., Shimada, K., Silva, D., Sinclair, B., Spelling, S., Stupka, E., Sugiyasu, K., Sultana, R., Takenaka, Y., Takaki, K., Tammoja, K., Tan, S.L., Tang, S., Taylor, M.S., Tegner, J., Teichmann, S.A., Ueda, H., van Nimwegen, E., Verardo, R., Wei, C.L., Yagi, K., Yamashita, H., Zdobych, E., Zhu, S., Zimmer, A., Hilde, M., Bult, C., Grimmond, S.M., Teasdale, R.D., Liu, B.T., Brusic, V., Quackenbush, J., Wahlstedt, C., Mattick, J.S., Hume, D.A., Kato, S., Sasaki, D., Tomaru, Y., Fukuda, S., Kanamori, K., Katayama, M., Suzuki, M., Aoki, J., Arakawa, T., Iida, J., Imanura, K., Itoh, M., Kato, T., Kawai, J., Kawasawa, N., Kawashima, T., Kojima, M., Kondo, S., Konno, H., Nakano, K., Niimura, N., Nishio, T., Okada, M., Plessey, C., Shibata, K., Shiraki, T., Suzuki, S., Tagami, M., Waki, K., Watanabe, A., Okamura-Oho, Y., Suzuki, H., Kawai, J., and Hayashizaki, Y.
CONSORTM
PANTOM Consortium
The transcriptional landscape of the mammalian genome
Science 309 (5740), 1559-1563 (2005)
- REFERENCE
AUTHORS
TITLE
JOURNAL
PUBMED
16141072
Katayama, S., Tomaru, Y., Kasukawa, T., Waki, K., Nakamishi, M., Nakamura, M., Nishida, H., Yag, C.C., Suzuki, M., Kawai, J., Suzuki, H., Carninci, P., Hayashizaki, Y., Wells, C., Frith, M., Ravasi, T., Pang, K.C., Hallinan, J., Mattick, J., Hume, D.A., Lipovich, L., Batalov, S., Engstrom, P.G., Mizuno, Y., Feghli, M.A., Sandoz, A., Chalk, A.M., Mottagui-Tabar, S., Liang, Z., Lenhard, B., and Wahlstedt, C.
CONSORTM
RIKEN Genome Exploration Research Group
Antisense transcription in the mammalian transcriptome
Science 309 (5740), 1564-1566 (2005)
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TITLE
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PUBMED
16141073
8 (baaes 1 to 4150)
Arakawa, T., Carninci, P., Fukuda, S., Hashizume, W., Hayashida, K., Hori, F., Iida, J., Imanura, K., Imokani, K., Itoh, M., Kanagawa, S., Kawai, J., Kojima, M., Konno, H., Murata, M., Nakamura, M., Niimura, N., Nishiyori, H., Nomura, K., Ohno, M., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shiraki, T., Tagami, M., Tagami, Y., Waki, K., Watanabe, A., Muramatsu, M., and Hayashizaki, Y.
Direct Submission

JOURNAL

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COMMENT

cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. Please visit our web site for further details. URL: http://genome.gsc.riken.jp/ URL: http://fantom.gsc.riken.jp/.

FEATURES

SOURCE

1. 4150
/organism="Mus musculus"
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RESULT 9 AKI63495 3761 bp mRNA linear HTC 21-SBP-2005

LOCUS AKI63495

DEFINITION Mus musculus adult male corpora quadrigemina cDNA, RIKEN full-length enriched library, clone:B30310M21 product:fibroblast growth factor receptor 3, full insert sequence.

ACCESSION AKI63495.1 GI:74200956

VERSION AKI63495

KEYWORDS HTC; CAP trapper.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE 1 Bukacynska, Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Muridae; Murinae; Mus.

REFERENCE 2 Carninci, P. and Hayashizaki, Y. High-efficiency full-length cDNA cloning Meth. Enzymol. 303, 19-44 (1999)

REFERENCE 3 10349636

TITLE Carninci, P. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)

JOURNAL PUBLISHED 11042159

REFERENCE AUTHORS

TITLE RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer

JOURNAL PUBLISHED Genome Res. 10 (11), 1757-1771 (2000)

REFERENCE 11076861

CONSRMT 4

TITLE Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y., Aikawa, T., Hara, A., Fukunishi, Y., Komoto, H., Adachi, J., Fukuda, S., Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamana, I., Saito, T., Okazaki, Y., Goto, T., Bono, H., Kaubakawa, T., Saito, R., Kadota, K., Matsuda, H., Ashburner, M., Batilov, S., Casavant, T., Fleschmann, W., Gaasterland, T., Gissi, C., King, B., Kochiwa, H., Kneissl, P., Lewis, S., Matsuo, Y., Nishida, I., Pesole, G., Quackenbush, J., Schriml, L.M., Staudt, F., Suzuki, R., Tomita, M., Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H., Balderelli, R., Barsh, G., Blake, J., Bottelli, D., Bottinga, N., Carninci, P., de Bona, M., Brownstein, M., Bult, C., Fletcher, C., Fujita, M., Gariboldi, M., Gustinich, S., Hill, D., Hofmann, M., Hume, D.A., Kamiya, M., Lee, N.H., Lyons, P., Marchionni, L., Mashima, J., Mazzarelli, J., Mombert, P., Nordone, P., Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H., Sato, K., Schombach, C., Seye, T., Shibata, Y., Storch, K.F., Suzuki, H., Toyo-oka, K., Wang, K.H., Weitz, C., Whitaker, C., Wilming, L., Wynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawai, J., Kontsuki, S., and Hayashizaki, Y.

CONSRMT 5

TITLE RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium

JOURNAL PUBLISHED Functional annotation of a full-length mouse cDNA collection Nature 409 (6821), 685-690 (2001)

REFERENCE 11217851

CONSRMT 5

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CONSRMT 6

TITLE FANTOM Consortium

JOURNAL PUBLISHED Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs Nature 420 (6915), 563-573 (2002)

REFERENCE 1246851

CONSRMT 6

TITLE Carninci, P., Kasukawa, T., Katayama, S., Gough, J., Fritsch, M.C., Maeda, N., Oyama, R., Ravasi, T., Lenhard, B., Wells, C., Kodzius, R., Shimokawa, K., Bajic, V.B., Brenner, S.E., Batilov, S., Forrest, A.R., Zavolan, M., Davis, M.J., Wilming, L.G., Aldins, V., Allen, J.E., Ambesi-Impombato, A., Apweiler, R., Auraliy, R.N., Bailey, T.L., Banal, K.P., Baxter, L., Beisel, K.W., Bersano, P., Bono, H., Chalk, A.M., Chiu, K.P., Choudhary, V., Christoffels, A., Clutterbuck, D.R., Croce, M.L., Dalla, E., Dalymp, B.P., de Bono, B., Della Gatta, G., di Bernardo, D., Down, T., Engstrom, P., Fagiolini, M., Faulkner, G.,

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 Plessy,C., Shibata,K., Shiraki,T., Suzuki,S., Tagami,M., Waki,K.,
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 FANTOM Consortium
 The transcriptional landscape of the mammalian genome
 Science 309 (5740), 1559-1563 (2005)
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 Katayama,S., Tomaru,Y., Kasukawa,T., Waki,K., Nakanishi,M.,
 Nakamura,M., Nishide,H., Yag,C.C., Suzuki,M., Kawai,J., Suzuki,H.,
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 Chalk,A.M., Motegui-Tabar,S., Liang,Z., Lenhard,B. and
 Wahlested,C.
 RIKEN Genome Exploration Research Group
 Antisense transcription in the mammalian transcriptome
 Science 309 (5740), 1564-1566 (2005)
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 8 (bases 1 to 3761)
 Arakawa,T., Carninci,P., Fukuda,S., Hashizume,W., Hayashida,K.,
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 Shibata,K., Shiraki,T., Tagami,M., Tagami,Y., Waki,K., Watanuki,A.,
 Muramatsu,M. and Hayashizaki,Y.
 Direct Submission
 Submitted (14-APR-2004) Yoshihide Hayashizaki, The Institute of
 Physical and Chemical Research (RIKEN), Laboratory for Genome
 Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
 RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama
 Kanagawa, 230-0045, Japan (E-mail:genome-res@gs.c.riken.jp,
 URL: http://genome.gsc.riken.jp/, Tel:81-45-503-9222,
 Fax:81-45-503-9216)
 COMMENT
 cDNA library was prepared and sequenced in Mouse Genome
 Encyclopeda Project of Genome Exploration Research Group in Riken
 Genomic Sciences Center and Genome Science Laboratory in RIKEN.
 Division of Experimental Animal Research in Riken contributed to
 prepare mouse tissues.
 Please visit our web site for further details.
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Query Match 29.2%; Score 905.4; DB 6; Length 3761;

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DB 481 TTGTTCTTCAGAGATGATGATGTTCTGTTTCTTCAGAACCCCATGCTTACGAACATGCTT 540
QY 2848 TCTCTAGATTCACATTAACGAGAGTTTAAACATGAATGATGTTGTCGCTGCTGCTC 2907
DB 541 TCTCTAGATTCACATTAACGAGAGTTTAAACATGAATGATGTTGTCGCTGCTGCTGCTC 600
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DB 601 CCAAAACAGAGACGAGCTGGGAACTAGCTACACTGAGAGGAGACCAATGCTCCCAAG 660
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DB 661 CTGTTGTTCTCCACTTGTATATATATGATCAGAGAGTAAATTAATGAGAAAGTAAATCAGC 720
QY 3028 ATATGTGTAAGATTTATACATGTTGAAAACTTGTATCTTCCCGAGGAGG--AGAAAG 3085
DB 721 ATATGTGTAAGATTTATACATGTTGAAAACTTGTATCTTCCCGAGGAGGAGAAAG 780
QY 3086 GTTCTGGAGCAGTGGACTGC 3106
DB 781 TTTCTGGAGCAGTGGACTGC 801

RESULT 11
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DEFINITION AU132307 NT2RP3 Homo sapiens cDNA clone NT2RP3004190 5', mRNA
sequence.
ACCESSION AU132307
VERSION AU132307.1 GI:10992661
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
1 (bases 1 to 803)
Kimura, K., Wakamatsu, A., Suzuki, Y., Ota, T., Nishikawa, T.,
Yamashita, R., Yamamoto, D., Sekine, M., Tsuritani, K., Makaguri, H.,
Ishii, S., Sugiyama, T., Saito, K., Isono, Y., Irie, K., Kushida, N.,
Yoneyama, T., Otsuka, R., Kanda, K., Yokoi, T., Kondo, H., Wagaitsuma, M.,
Murakawa, K., Ishida, S., Ishibashi, T., Takahashi, Fujii, A.,
Tanase, T., Nagai, K., Kikuchi, H., Nakai, K., Isogai, T. and Sugano, S.
Diversification of Transcriptional Modulation: Large-scale
Identification and Characterization of Putative Alternative
Promoters of Human Genes

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JOURNAL Genome Res. 16 (1), 55-65 (2006)
PUBMED 16344560
COMMENT Contact: Takao Isogai
FLJ Project (HRI Team)
Helix Research Institute
2-6-7 Kazusa-Kamatari, Kisarazu, Chiba, 292-0818, Japan
Tel: 81-438-52-3975
Fax: 81-438-52-3986
Email: flj-cdna@nifty.com
HRI human cDNA project; 5'- & 3'-end one pass sequencing; Helix
Research Institute; cDNA library construction; Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
FEATURES
Source Location/Qualifiers
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/clone_id="NT2"
/clone_lib="NT2RP3"
/notes="Vector: pME18SPJ3; mRNA from NT2 neuronal precursor
cells after 2-weeks retinoic acid (RA) induction"
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Best Local Similarity 98.1%; Pred. No. 3.1e-211;
Matches 788; Conservative 0; Mismatches 12; Indels 3; Gaps 2;
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DB 61 AGACTTGAAGCAGCCAGCCGCTGTGCAACAAGCTGACCAAGATATCCCTCGGAGACA 120
QY 1702 GGTAAAGTTTGGCTGATGTTCACTCTCTCATGAACTCCCAACACCCCGTGGAGGAT 1761
DB 121 GGTAAAGTTTGGCTGATGTTCACTCTCTCATGAACTCCCAACACCCCGTGGAGGAT 180
QY 1762 AACAAACGCTCTCTTCAACGAGACACCCCATGCTGAGGGGTCTCGAGTATGA 1821
DB 181 AACAAACGCTCTCTTCAACGAGACACCCCATGCTGAGGGGTCTCGAGTATGA 240
QY 1822 ACTTCCAGAGGACCCAAATGAGATTCCAAAGATTAAGCTGACACTGGCAAGCCCTT 1881
DB 241 ACTTCCAGAGGACCCAAATGAGATTCCAAAGATTAAGCTGACACTGGCAAGCCCTT 300
QY 1882 GGGAGAGGTTGCTTTGGGCAAGTGTATGGCCGAGAGCATGGGAATTTGACAAAGCAA 1941
DB 301 GGGAGAGGTTGCTTTGGGCAAGTGTATGGCCGAGAGCAATGGGAATTTGACAAAGCAA 360
QY 1942 GCCCAAGAGGCGGTCACCGTGGCCGTGAAGATGTTGAAAGATGTCACAGAGAAAGA 2001
DB 361 GCCCAAGAGGCGGTCACCGTGGCCGTGAAGATGTTGAAAGATGTCACAGAGAAAGA 420
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QY 2242 CTACCACTGGCCAGACGATGAGTACTTGGCTTCCCAAAATGATTCATCGAGATT 2301
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 DB 720 AACAGCCAGAAATGTTTGGTAAACAGAAACATGATGAAATAGCAGACTTTGGAC 779
 QY 2360 CTCGCCAGATATCAACAATAT 2382
 DB 780 TCGNCCAGATNTCAACAATT 802
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 LOCUS 1097231 MARC 4PIG Sus scrofa cDNA 5', mRNA sequence.
 ACCESSION DNI02322
 VERSION DNI02322.1 GI:59775098
 KEYWORDS EST.
 SOURCE Sus scrofa (pig)
 ORGANISM Sus scrofa
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suidae; Suidae;
 Sus.
 1 (bases 1 to 898)
 Smith,T.P.L., Freking,B.A., Ford,J.J., Vallet,J.L., Wise,T.A.,
 Nomenan,D.J., Wray,J.B. and Keefe,J.W.
 Porcine EST collection using a normalized library constructed from
 embryos representing early developmental stages
 Unpublished (2003)
 Contact: Smith TPL
 USDA, ARS, US Meat Animal Research Center
 PO Box 166, Clay Center, NE 68933-0166, USA
 Tel: 402 762 4366
 Fax: 402 762 4390
 Email: smith@email.marc.usda.gov
 Single pass sequencing. Bases called with phred v0.020425.c and
 trimmed with the aid of the trim_alt option. Vector identified with
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 Plate: TM6072 row: 1 column: 4
 Seq primer: GTAAATCGACTCCTATAGG.
 Location/Qualifiers
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 /lab_host="DH10B"
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 Best Local Similarity 90.1%; Pred. No. 4.9e-210;
 Matches 809; Conservative 0; Mismatches 89; Indels 0; Gaps 0;
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 DB 61 TCATAGTTAGTATGCTCTTAAGCACTCCGAGATTAACCTCCGAGCCCGGAGCCAC 120
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 DB 121 CCGGAGTGAAGTACTCTTATGACATTAACCGTGTCTCTTGAAGAGCAGATGACTTCA 180
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DB 181 ACTGTGTATGACACTTACCACTGCGCAGAGAGATGATCTTGGCTTCCCAAAAT 240
 QY 2286 GTATTCATCGAGATTTAGCAGCCAGAAATGTTTGGTAAACAGAAACATGATGAA 2345
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 QY 2346 TAGCAGACTTTGGAATGCGCAGAGATATCAATATATGACTATACAAAAGACCA 2405
 DB 301 TAGCAGACTTTGGAATGCGCAGAGATATCAATATATGACTATACAAAAGACCA 360
 QY 2406 ATGGCGGCTTCAGTCAAGTGAATGCTCCAGAAACCCCTGTTTATGATAGTATAC 2465
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 DB 841 GAATGACGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 898
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 LOCUS AGENCOURT_14553523 NIA Human H1 Embryonic Stem Cell cDNA Library
 DEFINITION (Long) Homo sapiens cDNA clone IMAGE:30428791 5', mRNA sequence.
 ACCESSION CD643272
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 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Hominiidae; Homo.
 1 (bases 1 to 757)
 NIH-MGC http://mgi.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Daniela S. Gerhard, Ph.D.
 Office of Cancer Genomics / NIH
 National Cancer Institute
 Bldg. 31 Rm10A07 Bethesda, MD 20892
 Email: cgabbs-remail.nih.gov
 Tissue Procurement: Irene Gins and Mahendra Rao, NIA
 cDNA Library Preparation: Yulan Piao and Minoru Ko
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC c lome distribution information
 http://image.llnl.gov
 Plate: NDAM518 row: 9 column: 08
 High quality sequence stop: 676.
 Location/Qualifiers

FEATURES

SOURCE

1. 757
 /organism="Homo sapiens"
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 /issue_type="Embryonic Stem cells"
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 /clone_1ib="NIA Human H1 Embryonic Stem Cell cDNA library (long)"

/note="Vector: pCMV-Sport6; Site_1: NotI; Site_2: SalI; This is a long-transcript enriched cDNA library (Genome Res. 11: 1553-1558 (2001). [PMID: 1154199]) from WA01 cell line. Undifferentiated human ES cell line WA01/H1 was obtained from WiCell Research Institute, Inc., Madison, WI, cultured according to their instructions, on MBP feeders. They formed round colonies with defined edges and were positive for alkaline phosphatase, SSEA-4, OCT3, OCT4, REX1, UTE, TERT, SOX2, CX43 and CX45. They are negative for GATA2, GATA4, PDX1, NCAM, MSX1, FLK3, SSEA-1, TUBB3, NES, GFAP, and EOMES. When confluent (18-10 days after plating), the ES cells from 4 X 6 cm dishes were treated with 1 mg/ml collagenase, type IV (Invitrogen/GIBCO) for 5-10 min and gently scraped off with 5 ml pipette. Protocol ref: Genome Res. 11: 1553-1558 (2001). [PMID:1154199]) Double-stranded cDNAs were synthesized with an Oligo(dT) primer (Invitrogen: 5'-pGACAGTCTAGATCGGAGCGCGCCCTTTTCTTTT-3') from 3.4g of total RNA, treated with T4 DNA polymerase, and purified by ethanol-precipitation. The cDNAs were ligated to lome-linker lI-SalI, purified by phenol/chloroform extraction, and separated from free linkers by Centricon-100 column. Then, the cDNAs were amplified by long-range high fidelity PCR using Ex Taq polymerase (Takara) with a primer SalI-4-S for 25 cycles. The products were purified by phenol/chloroform extraction and Centricon-100 column. The cDNAs were digested with SalI and NotI enzymes and cloned into SalI/NotI site of pCMV-Sport6 plasmid vector. The average insert size is about 3.6kb."

ORIGIN

Query Match 23.7%; Score 735; DB 5; Length 757;
 Best Local Similarity 98.3%; Pred. No. 5.4e-204;
 Matches 741; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

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 4 GGTATCCCAACCGCTCTTCAACGGCAGACACCCCAAGCTGGAGGGGTCTCCGAGTA 63

1819 TGAACCTTCAGAGAGACCCAAATGGAGTTCACAGAGATAGCTGACACTGGCAAGCC 1878
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 64 TGAACCTTCAGAGAGACCCAAATGGAGTTCACAGAGATAGCTGACACTGGCAAGCC 123

1879 CCTGGAGAGAGGTGCTTTGGCAAGTGTCTATGGCGAAGAGAGTGGGAATTTGACAAAGA 1938
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 124 CCGGAGAGAGGTGCTTTGGCAAGTGTCTATGGCGAAGAGAGTGGGAATTTGACAAAGA 183

1939 CAAGCCCAAGAGAGCGGTGACCGTGGCCGTGAAGATTTGAAAGATGATGCCACAGAGAA 1998
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 184 CAAGCCCAAGAGAGCGGTGACCGTGGCCGTGAAGATTTGAAAGATGATGCCACAGAGAA 243

1999 AGACCTTCTGATCTGGGTGTCAGAGATGAGATGATGATGATGGGAAACACAGAA 2058
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 244 AGACCTTCTGATCTGGGTGTCAGAGATGAGATGATGATGATGGGAAACACAGAA 303

OY 2059 TATCATTAATCTTTTGGAGCTTGACACAGATAGGGCTCTGANTGCTAAGTTGAGTA 2118
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 DB 304 TATCATTAATCTTTTGGAGCTTGACACAGATAGGGCTCTCTATGTCATAGTTGAGTA 363

OY 2119 TGCCTTAAGAGCAACCTCCGAGATACCTCCGAGCCCGAGGCCACCGGAGATGAGTA 2178
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 DB 364 TGCCTTAAGAGCAACCTCCGAGATACCTCCGAGCCCGAGGCCACCGGAGATGAGTA 423

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 DB 424 CTCCTATGACATTAAACCGTGTCTCTGAGAGACAGATACCTTCAAGACCTTGTGTATG 483

OY 2239 CACTTACAGCTGGCCGAGACGAGATGAGTCTTGGCTTCCCAAAATGATTTATCGAGA 2298
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 DB 484 CACTTACAGCTGGCCGAGACGAGATGAGTCTTGGCTTCCCAAAATGATTTATCGAGA 543

OY 2299 TTTAGCAGCCGAGATATTTTGTATACAGAAACATGTGATGAAATAGCAGACTTTGG 2358
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 DB 544 TTTAGCAGCCGAGATATTTTGTATACAGAAACATGTGATGAAATAGCAGACTTTGG 603

OY 2359 ACTGCGCAGAGATATCAACATATATAGACTATTTACAAAAGACCAACATGGCGCTTCC 2418
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 DB 604 ACTGCGCAGAGATATCAACATATATAGACTATTTACAAAAGACCAACATGGCGCTTCC 663

OY 2419 AGTCAGATGATGCTCCAGAGCCCTTTGATAGATATACCTGATCAGATGATGT 2478
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 DB 664 AGTCAGATGATGCTCCAGAGCCCTTTGATAGATATACCTGATCAGATGATGT 723

OY 2479 CTGGTCTCTCGGGGTGTTAATGTGGAGATCTTC 2512
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 DB 724 CTGGTCTCTCGGGGTGTTAATGTGGAGATCTTC 757

RESULT 14
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 DEFINITION
 Mus musculus 13 days embryo lung cDNA, RIKEN full-length enriched library, clone: P430001102 product: fibroblast growth factor receptor 4, full insert sequence.

ACCESSION
 AK084850
 VERSION
 AK084850.1 GI:26351310
 KEYWORDS
 HTC; CAP trapper.

SOURCE
 Mus musculus (house mouse)

ORGANISM
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidae; Muridae; Mus.

REFERENCE
 1 Carninci, P. and Hayashizaki, Y.
 High-efficiency full-length cDNA cloning
 Meth. Enzymol. 303, 19-44 (1999)
 10349636

REFERENCE
 2
 11042159

TITLE
 JOURNAL
 PUBMED
 REFERENCE
 AUTHORS

3
 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
 Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
 Genome Res. 10 (10), 1617-1630 (2000)

TITLE
 JOURNAL
 PUBMED
 REFERENCE

4
 Shibata, K., Itoh, M., Aizawa, K., Nagao, S., Sasaki, H., Carninci, P., Kono, H., Akiyama, U., Nishi, K., Kiteunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishino, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watanuki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsui, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kita, A. and Hayashizaki, Y.
 RIKEN integrated sequence analysis (RISA) system-384-format
 sequencing pipeline with 384 multiplexillary sequencer
 Genome Res. 10 (11), 1757-1771 (2000)
 11076861

AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the PANTOM Consortium.

TITLE Functional annotation of a full-length mouse cDNA collection

JOURNAL Nature 409, 685-690 (2001)

REFERENCE 5

AUTHORS The PANTOM Consortium, the RIKEN Genome Exploration Research Group Phase I and II Team.

TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

JOURNAL Nature 420, 563-573 (2002)

REFERENCE 6

AUTHORS RIKEN Genome Exploration Research Group, Genome Science Group (Genome Network Core Team) and the PANTOM Consortium.

TITLE Antisense transcription in the Mammalian Transcriptome

JOURNAL Science 309, 1564-1566 (2005)

REFERENCE 7

AUTHORS The PANTOM Consortium, Riken Genome Exploration Research Group and Genome Science Group (Genome Network Project Core Group).

TITLE The Transcriptional Landscape of the Mammalian Genome

JOURNAL Science 309, 1559-1563 (2005)

REFERENCE 8 (bases 1 to 3146)

AUTHORS Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hagiwara, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hirooka, T., Hirozane, T., Horii, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, T., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M., and Hayashizaki, Y.

TITLE Direct Submission

JOURNAL Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan (E-mail: genome-res@gsr.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

COMMENT cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

URL: http://genome.gsc.riken.jp/

URL: http://fantom.gsc.riken.jp/

URL: http://fantom.qualifiers

FEATURES

source

1. 3146

/organism="Mus musculus"

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/strain="C57BL/6J"

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/db_xref="taxon:10090"

/clone="D430001L02"

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/dev_stage="13 days embryo"

163. 2362

/note="unmated protein product; fibroblast growth factor receptor 4 [MGI:95525, evidence: Direct assignment] putative"

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/codon_start=1

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CDS

ORIGIN

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polyA_site

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/note="putative"

3146

/note="putative"

Query Match 23.4%; Score 728; DB 6; Length 3146;

Best Local Similarity 61.4%; Pred. No. 1e-201;

Matches 1270; Conservative 0; Mismatches 770; Indels 30; Gaps 5;

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491 TTACGTTGCTATGATGATGATCTCTTAACTCCTCATGATATGATGAGCCCAAGAC 550

837 CCGAAGATTGTCAGTGAAGACATGAACAAGAGACACATTAAGTGAACACAG 896

551 TCAGACGCTCTCGATGTCATGTCATCCACAGAGACACCTTAAGTGAACACCC 610

897 AAAAGTGAAGAGCGGCTCATGCTGTCGCGGCAACCTGTCAGAGTTGCTGTC 956

611 AACGATGAGAGAAAGTCAATGATGATGATGATGATGATGATGATGATGATG 670

957 CAGCGCGGAGGAGAACCAAGCCACATGCGGTCGAGAAACGAGAGAGATTAGC 1016

671 CAGCTGCAAGAGAACCAAGCTTACCTACCTGCTCAAGATGATGATGATGATG 730

1017 AGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1076

731 GGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 790

1077 GTGTGTCCATCTGACAAAGGAAATTAATTAATTAATTAATTAATTAATTA 1136

791 GTGTGTCCATCTGACAAAGGAAATTAATTAATTAATTAATTAATTAATTA 850

1137 TCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1196

851 TTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 910

1197 CCGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1256

911 CCGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 970

1257 TTTACAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1316

971 TTTACAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1030

1317 AATACGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1376

1031 GCTTCGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1090

1377 CCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1436

1091 CCGAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1150

1437 GTAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1496

1151 GTTCGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1210

1497 AACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1556

1211 A-----GGAAGATGATGATGATGATGATGATGATGATGATGATGATGATG 1258

1557 CCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1616

Db	1259	ATATCATCTCTGTATGTATACAGAGCTCACTGGTTCTGTTGTGCTCTGCTGCTGGCCGGGG	1318
Oy	1617	GAATGAGAACAACGACCAAGAAAGCCAGACTTTACAGACGCAAGCCGGCTGTGCAAGCTGA	1676
Db	1319	TGTATCATCTGGCAAGTCAATCCGTGGCCACTACTCTGCGACGCTGTCACTATACAAAGC	1378
Oy	1677	CCAAACGATCCCCCTGTGGAGACAGGTAAACGTTTGCGCTGAGTCCAGCTCCCTCATGA	1736
Db	1319	TGTCCCGTTTCCCTTTGGCCCCGACG-----TTCTCTTTGGATTCAGAGTCTCTGGCA	1432
Oy	1737	ACTCCAAACCCCGCTGGTGAAGATTAACAACGCTCTCTTTCAACGGCAGACACCCCA	1796
Db	1433	AGTCAAGTTTGTCCCTGTGGCG-----AGGTGTCCGTCTCTCCCTCCAGCGGCCGCGCT	1486
Oy	1797	TGCTGGCAGGGGCTCTCCGATATGAACTTCCAGAGAACCCAAATATGGAGTTTCAAGAG	1856
Db	1487	TGCTACAGGGCTTGTGAATCTAGACCTGCTCTCGATCCGCTTTGGGAATTTCCCGGG	1546
Oy	1857	ATATGCTGACACTGGGCAAGCCCTCTGGAGAAAGTTGCTTTTGGCAAGTGTCAATGGCGG	1916
Db	1547	ACAGTTGTGTGTGGAAAGCCCTCGGGTGAAGGGCTGTTTGGGCAAGTGTGTGTGACAG	1606
Oy	1917	AAGCAGTGGGAATTGACAAAGCAAGCCCAAGAGCGGTCAACGTTGCGGTGAAGATGT	1976
Db	1607	AGGCTTTTGTATGTGATCTCTCCGGGCCGACCAACAGCAGACGTTGCTGTGAAGATGC	1666
Oy	1977	TGAATGATGATATCCACAGAGAAAGACTTTTGTGATCTGTGTCAGAGATGAGATGATGA	2036
Db	1667	TGAAAGACATATCTCTCCGACAAAGATTTGGCAGACCTGTCTCCGAGATGGAGGTATGA	1726
Oy	2037	AGATGATTTGGGAAACAACAAGATATCATTAATCTTTTGGAGCTGCACACAGATGGCG	2096
Db	1727	AGCTATATGGAGAAACAACAAGATCATCAACCTGTCTGGTGTCTGCACTTCAGAGAAAGGC	1786
Oy	2097	CTCTGTATGTCACTAGTTGATGTGCTCTTAAGGCAACCTCCGAGAAATACCTCCGAGCCC	2156
Db	1787	CCCTGTACGTATTTGTGAATGTGCGCCAGAGGAAACCTTCGGGAATTCCTCCGTGCC	1846
Oy	2157	GGAGGCCACCCGGGATGGAATCTCTATGACATTAACCGTGTCTTGAGGACGATGA	2216
Db	1847	GGCGCCCCCAGGCGCTGATCTCAACCTGTATGACCTTCGAGAGACGACAAAGAACACTCT	1906
Oy	2217	CCTTCAAGGACTTTGGTGTCAAGCACTTAACAGCTGGCCAGACGATGAGATTTGGCTT	2276
Db	1907	CCTTCCCGCCCTATGTCTCTGTGTCTACACAGTGGCCCGAGGACATGAGATCTGAAGT	1966
Oy	2277	CCCAAAATATATATCGAGATTTAGAGACGACGAATATGTTTGGTACAGAAAACATG	2336
Db	1967	CTCGGAATGATCAACCGGGACCTGGGCTGCCGAATGTGTGGTGAACGAGATGATG	2026
Oy	2337	TGATGAAATAGCAACTTTTGGACTTCGCCAGAGATATCAACATATATGACTATTTACAAA	2396
Db	2027	TGATGAAGTATCTCTACTTTTGGGCGGCAACGTGTGTCTCACACATGACTACTATATAGA	2086
Oy	2397	AGACCAACCAATGGGGGGCTTCAGTCAAGTGAATGGCTTCAGAAAGCCCTGTGTATAGAG	2456
Db	2087	AAACCAAGCAAGGCGCGCTGCCAGTCAATGATGGCTTCAGAGGCAATGTTTCACCGCG	2146
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Oy	2517	TAGGGGGCTCGCCATACCAAGGAAATTCGCTGAGAGAACTTTTAAGTGTGTGAAGAG	2576
Db	2207	TGCGGGGCTCCCATACCTTGCATATTCGAGTGAAGAGCTCTTCTCACTGTCTCGAGAG	2266
Oy	2577	GACACGAATGATTAAGCAGCAACTGCACCAAGAACTGTATCATGATGAAGAGCT	2636
Db	2267	GGACACAGATGAGAGGGGCCCAAACTGCGCTCAGAGCTGTATGGGCTAATGAGGGAGT	2326
Oy	2637	GTTTGCATCAATGCCCTCCACAGACCAAGTTCAAGCAGTTGGTAAACAATTGATC	2696
Db	2327	GCTGGACCAAGCCCATCTCAGAGGCTTATTAAGCAGCTGTGTGAAGCTCTGAG--	2384

Qy	2697	GAATTCCTCCTCTCACAACCAATGAGAAATCTTGACACCTCAGCCAACTCTCAAGAGT	2756
Db	2385	-CAAGGTCCTGGCTGCTGTCTCTTAAGAAGTACTTACCTCGCTGACCTTGACCCCT	2443
Qy	2757	ATTACACCTAGTATCCCTGACACAGAAGTCTTGTTCTTCAGAGATGATTTCTGTTTTT	2816
Db	2444	TTTCTCCCTCCAAATGGGAGATGCCGACGACACTGCTCTCCAG---TGACTGGTTTTCA	2500
Qy	2817	CTCCAGACCCCATGCTTACGACCAATGCC	2846
Db	2501	GCCACGACCTTGTGCCCCCTCGAGCCAGGCC	2530
RESULT 15			
AK081810			
LOCUS			
DEFINITION	AK081810	2218 bp	mRNA
			linear
			HTC 02-SEP-2005
			Mus musculus 16 days embryo head cDNA, RIKEN full-length enriched
			library, clone:c130078M18 product:fibroblast growth factor receptor
			2, full insert sequence.
ACCESSION	AK081810		
VERSION	AK081810.1	GI:26100195	
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SOURCE	Mus musculus (house mouse)		
ORGANISM	Mus musculus		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;		
	Sciurognathi; Muridae; Muridae; Murinae; Mus.		
REFERENCE			
AUTHORS	1	Carninci, P. and Hayashizaki, Y.	
TITLE		High-efficiency full-length cDNA cloning	
JOURNAL		Meth. Enzymol. 303, 19-44 (1999)	
PUBMED	10349636		
REFERENCE			
AUTHORS	2	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,	
		Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y.	
		Normalization and subtraction of cap-trapper-selected cDNAs to	
		prepare full-length cDNA libraries for rapid discovery of new genes	
		Genome Res. 10 (10), 1617-1630 (2000)	
JOURNAL	11042159		
PUBMED			
REFERENCE			
AUTHORS	3	Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,	
		Kono, H., Akiyama, J., Nishi, K., Kitanaka, T., Tashiro, H., Itoh, M.,	
		Sun, N., Ishii, Y., Nakamura, S., Hazama, M., Nishino, T., Harada, A.,	
		Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kasai, K.,	
		Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watabiki, M.,	
		Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J.,	
		Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.	
		RIKEN integrated sequence analysis (RISA) system-384-format	
		sequencing pipeline with 384 multicapillary sequencer	
		Genome Res. 10 (11), 1757-1771 (2000)	
JOURNAL	11076861		
PUBMED			
REFERENCE			
AUTHORS	4	The RIKEN Genome Exploration Research Group Phase II Team and the	
		FANTOM Consortium.	
		Functional annotation of a full-length mouse cDNA collection	
		Nature 409, 685-690 (2001)	
JOURNAL	5		
PUBMED			
REFERENCE			
AUTHORS		The FANTOM Consortium, the RIKEN Genome Exploration Research Group	
		Phase I and II Team.	
		Analysis of the mouse transcriptome based on functional annotation	
		of 60,770 full-length cDNAs	
		Nature 420, 563-573 (2002)	
JOURNAL	6		
PUBMED			
REFERENCE		RIKEN Genome Exploration Research Group, Genome Science Group	
		(Genome Network Core Team) and the FANTOM Consortium.	
		Antisense Transcription in the Mammalian Transcriptome	
		Science 309, 1564-1566 (2005)	
JOURNAL	7		
PUBMED			
REFERENCE		The FANTOM Consortium, Riken Genome Exploration Research Group and	
		Genome Science Group (Genome Network Project Core Group).	
		The Transcriptional Landscape of the Mammalian Genome	
		Science 309, 1559-1563 (2005)	
JOURNAL			
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REFERENCE			
AUTHORS			
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REFERENCE 8 (bases 1 to 2218)
 AUTHORS Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hirooka,T., Hirozane,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T., Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numata,C., Sakai,K., Sakazume,N., Okazaki,Y., Saito,R., Saitoh,H., Sekai,C., Shikata,T., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.

TITLE Direct Submission
 JOURNAL Submited (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan [E-mail:genome-res@gs.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216]

COMMENT cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
 Please visit our web site for further details.
 URL:http://genome.gsc.riken.jp/
 URL:http://fantom.gsc.riken.jp/
 Location/Qualifiers
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 /note="fibroblast growth factor receptor 2 (MGD|MG1:95523, evidence: Direct assignment)
 putative"

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 Best local Similarity 88.1%; Pred. No. 4,1e-199;
 Matches 817; Conservative 0; Mismatches 105; Indels 5; Gaps 3;

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 DB 1 ATGACATTAAACCGTGTCTCGAGAGCAATGACCTTCAAGACTTGTCTCAGCACTT 60

QY 2244 ACCAGCTGGCCAGACGATGAGTACTTGGCTCCCAAAAATGATTCATCGAGATTAG 2303
 DB 61 ACCAGCTGGCTAGAGCATGAGTACTTGGCTCCCAAAAATGATTCATCGAGATTAG 120

QY 2304 CAGCCAGAAATGTTTGTGTAACAGAAAACAATGTGTAATAATAGCACTTGAAGCTG 2363
 DB 121 CTGCCAGAAACGTGTGTGTAACAGAAAACAATGTGTAATAATAGCACTTGAAGCTG 180

QY 2364 CCAGAGATATCAACATATAGACTATTACAAAAAGACCAACCAATGGCG- GCTTCCAGTC 2422
 DB 181 CCAGAGATATCAACATATAGACTATTACAAAAAGACCAACCAATGGCGCTTCCAGTC 240

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 DB 241 AATGTAGTGGCTCCTGTAAGCCCTTTTGTAGAGTATACATCATCAGAGTATGCTGG 300

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 DB 301 TCCTTGCGGGGTGTTAAATGTGGAGATCTTCACTTTAGGGGGCTCACCCCTAACCCAGGGAAT 360

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 DB 361 CCGGTGAGGAACCTTTTAAGCTGTGTCAAGAGGACACAGATGACAGGCCACACAC 420

QY 2603 TGCACCAAGAACTGTACATGATGATGAGAGGACTGTGGATGACAGTCCCTCCAGAGA 2662
 DB 421 TGCACCAATGAACCTGTACATGATGATGAGAGGATGCTGGATGCTGTACCTCCAGAGA 480

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 DB 481 CCCAATTCAGCAAGTGTGTGTAAGAACTTGAATTCGAATTCCTGACCAACCAATGAG 540

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 DB 541 GAATCTTGGAGCTAGACCAAGCTCTCGAAGAGTATTCCTAGTTAACCTTGACACAAG 600

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 DB 601 AGCTCTGTCTTTCAGAGGAGATTCGTGTTTCTCCAGAACCCAGTCTTATGAACCC 660

QY 2843 TCCCTTCTCAGATATCCACATTAACGCAAGTGTAAACATGATGACTGTCTGCTCC 2902
 DB 661 TCCCTGCTCAGATATCCACATTAACGCAAGTGTAAACATGATGATGACTGTCTGCTCC 720

QY 2903 TGTCCCAAGCAGACAGCACTGGGACCTAGCTACACTGACAGAGGAGACCATGCTCC 2962
 DB 721 TGTCCCAAGCAGACAGCACTGGGACCTAGCTACACTGACAGAGGAGGCTGTGCTCC 780

QY 2963 CAGAGCT--TGTGTCTCACTGTATATATGATGATGACAGAGTAAATATTTGAAAG 3019
 DB 781 AAGAGCTGTGACAGCGCTCTCACTGTATATATGATGATGACAGAGTAAATATTTGAAAG 840

QY 3020 TAATGACATATGTGTAAAGATTATTAACGTTGAAAACCTTGTAACTTCCCGAGAGAGG 3079
 DB 841 TATTTGTCACTGTGTAAAGATTATTAACGTTGAAAACATGTTA--CTTAACAGAGAAAG 899

QY 3080 AAGAGGTTTTCGAGCAGTGAAGTGC 3106
 DB 900 AAGAGGTTTTCGATTAAGTGAAGTGC 926

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